



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122834

To: Patricia Patten (Leith)
Location: REM-3C04&3C3D11
Art Unit: 1654
Wednesday, May 26, 2004

Case Serial Number: 09/830964

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

122834

STIC-Biotech/ChemLib

From: STIC-ILL
Sent: Monday, May 24, 2004 3:47 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/830,964

CRFE

See below.

-----Original Message-----

From: Leith, Patricia
Sent: Monday, May 24, 2004 3:21 PM
To: STIC-ILL
Subject: 09/830,964

Please search SEQ ID NO. 1 of 09/830,964.

Thank you.

Patty Leith

US Patent and Trademark Office
Tech Center 1600
Biotechnology
Art Unit 1654
REM 3C04

(571) 272-0968

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: May 25, 2004, 11:21:39 ; Search time 184 Seconds
(without alignments)
875.265 Million cell updates/sec

title: US-09-830-964-1
effect score: 846
equences: 1 APPRLICDSRVLYLEAK.....SNFLRGKLYTGBACRTGD 165

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 6019581 seqs, 976053577 residues

total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%

Database : Pending Patents_AA_Main:*

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- 2: /cgn2_6/prodata/2/paa/US06 COMB.ppe.*
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- 32: /cgn2_6/prodata/2/paa/US107 COMB.ppe.*
- 33: /cgn2_6/prodata/2/paa/US60 COMB.ppe.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	846	100.0	165	1	PCT-US03-31974-73	Sequence 73, Appl
2	846	100.0	165	1	PCT-US99-26238-1	Sequence 1, Appl
3	846	100.0	165	1	PCT-US99-26240-1	Sequence 1, Appl
4	846	100.0	165	1	PCT-US99-26241-1	Sequence 1, Appl
5	846	100.0	165	18	US-09-426-566-1	Sequence 1, Appl
6	846	100.0	165	20	US-09-687-981-1	Sequence 1, Appl
7	846	100.0	165	23	US-09-830-964-1	Sequence 1, Appl
8	846	100.0	165	23	US-09-830-967-1	Sequence 1, Appl
9	846	100.0	165	23	US-09-830-968-1	Sequence 1, Appl
10	846	100.0	165	23	US-09-853-731-1	Sequence 1, Appl
11	846	100.0	165	23	US-09-854-018-1	Sequence 1, Appl
12	846	100.0	165	24	US-09-945-517-1	Sequence 1, Appl
13	846	100.0	165	26	US-10-014-363-1	Sequence 1, Appl
14	846	100.0	165	28	US-10-241-356-1	Sequence 1, Appl
15	846	100.0	165	28	US-10-293-551-1	Sequence 73, Appl
16	846	100.0	165	30	US-10-410-897-73	Sequence 73, Appl
17	846	100.0	165	30	US-10-410-913-73	Sequence 73, Appl
18	846	100.0	165	30	US-10-410-930-73	Sequence 73, Appl
19	846	100.0	165	30	US-10-410-945-73	Sequence 73, Appl
20	846	100.0	165	30	US-10-410-962-73	Sequence 73, Appl
21	846	100.0	165	30	US-10-410-980-73	Sequence 73, Appl
22	846	100.0	165	30	US-10-410-997-73	Sequence 73, Appl
23	846	100.0	165	30	US-10-411-012-73	Sequence 73, Appl
24	846	100.0	165	30	US-10-411-026-73	Sequence 73, Appl
25	846	100.0	165	30	US-10-411-037-73	Sequence 73, Appl
26	846	100.0	165	30	US-10-411-043-73	Sequence 73, Appl
27	846	100.0	165	30	US-10-411-044-73	Sequence 73, Appl
28	846	100.0	165	30	US-10-411-049-73	Sequence 73, Appl
29	846	100.0	165	32	US-10-706-701-1	Sequence 1, Appl
30	846	100.0	166	1	PCT-US98-14497-2	Sequence 2, Appl
31	846	100.0	166	3	US-07-766-964A-3	Sequence 3, Appl
32	846	100.0	166	4	US-08-049-802-37	Sequence 37, Appl
33	846	100.0	166	6	US-08-223-283-7	Sequence 7, Appl
34	846	100.0	166	6	US-08-223-283A-7	Sequence 7, Appl
35	846	100.0	166	6	US-08-232-533-37	Sequence 37, Appl
36	846	100.0	166	6	US-08-249-376-7	Sequence 7, Appl
37	846	100.0	166	6	US-08-249-376A-7	Sequence 7, Appl
38	846	100.0	166	7	US-08-249-376B-7	Sequence 7, Appl
39	846	100.0	166	7	US-08-374-540-7	Sequence 7, Appl
40	846	100.0	166	8	US-08-422-020-7	Sequence 7, Appl
41	846	100.0	166	8	US-08-422-020A-7	Sequence 7, Appl
42	846	100.0	166	8	US-08-422-194-7	Sequence 7, Appl
43	846	100.0	166	8	US-08-422-194A-7	Sequence 7, Appl
44	846	100.0	166	8	US-08-422-548-7	Sequence 7, Appl
45	846	100.0	166	8	US-08-422-727-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
PCT-US03-31974-73
; GENERAL INFORMATION:
; Sequence 73, Application PC/TUS0331974

; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn

; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi

; APPLICANT: Bove, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN

; FILE REFERENCE: 040853-01-5083WO
; CURRENT APPLICATION NUMBER: PCT/US03/31974

; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/32263

; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/297,994

; PRIOR FILING DATE: 2002-11-5
; PRIOR APPLICATION NUMBER: US 10/360,770

; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 10/369,779

REMODELING AND GLYCOCONGUATION OF

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; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-31974-73

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Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKAEIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKAEIS 120

QY 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 2
PCT-US99-26238-1
; Sequence 1, Application PC/TUS99926238
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1792.002PC02
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: PCT/US99/26238
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05609
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26238-1

Query Match          100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKAEIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKAEIS 120

QY 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 3
PCT-US99-26240-1
; Sequence 1, Application PC/TUS99926240
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; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells Producing Recombinant Hum
; TITLE OF INVENTION: Erythropoietin
; FILE REFERENCE: 1792.004PC02
; CURRENT APPLICATION NUMBER: PCT/US99/26240
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: AR 99-01-00681
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05611
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26240-1

Query Match          100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRITITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 4
PCT-US99-26241-1
; Sequence 1, Application PC/TUS99926241
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Methods of Purifying Recombinant Human Erythropoietin from Cell
; TITLE OF INVENTION: Culture Supernatants
; FILE REFERENCE: 1792.003PC02
; CURRENT APPLICATION NUMBER: PCT/US99/26241
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: AR 99-01-00680
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05610
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26241-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-89;
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121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165
121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165

RESULT 5

S-09-426-566-1
Sequence 1, Application US/09426566
GENERAL INFORMATION:
APPLICANT: Burke, Paul
APPLICANT: Klumb, Lisa
APPLICANT: Murphy, Keith
APPLICANT: Herberger, John
APPLICANT: French, Donna
TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY
TITLE OF INVENTION: OF NOVEL ERYTHROPOIETIN STIMULATING PROTEIN
FILE REFERENCE: A-626
CURRENT APPLICATION NUMBER: US/09/426,566
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: HUMAN
US-09-426-566-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165

RESULT 6

US-09-687-981-1
Sequence 1, Application US/09687981
GENERAL INFORMATION:
APPLICANT: Burke, Paul
APPLICANT: Klumb, Lisa
APPLICANT: Murphy, Keith
APPLICANT: Herberger, John
APPLICANT: French, Donna
TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY OF NOVEL
TITLE OF INVENTION: ERYTHROPOIETIN STIMULATING PROTEIN
FILE REFERENCE: A-626A
CURRENT APPLICATION NUMBER: US/09/687,981
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/426,566
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-687-981-1

Query Match 100.0%; Score 846; DB 20; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165
121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165

RESULT 7

US-09-830-964-1
Sequence 1, Application US/09830964
GENERAL INFORMATION:
APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Criscuolo, Marcelo
APPLICANT: Melo, Carlos
APPLICANT: Vidal, Juan Alejandro
TITLE OF INVENTION: Methods of Purifying Recombinant Human
TITLE OF INVENTION: Erythropoietin from Cell Culture Supernatants
FILE REFERENCE: 1909.0030002
CURRENT APPLICATION NUMBER: US/09/830,964
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: AR 99-01-00680
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: AR 98-01-05610
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-830-964-1

Query Match 100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKRMVEVGQA 60
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165
121 PPDAASAAPLRTITADTFKFLFRVYGNFRLGKLYTGEACRTGD 165

RESULT 8

US-09-830-967-1
Sequence 1, Application US/09830967
GENERAL INFORMATION:
APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Criscuolo, Marcelo
APPLICANT: Melo, Carlos
APPLICANT: Vidal, Juan Alejandro
TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
FILE REFERENCE: 1909.0020002
CURRENT APPLICATION NUMBER: US/09/830,967
CURRENT FILING DATE: 1999-11-08

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; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 23; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 9
US-09-830-968-1
; Sequence 1, Application US/09830968
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells
; TITLE OF INVENTION: Producing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0040002
; CURRENT APPLICATION NUMBER: US/09/830,968
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00681
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05611
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-968-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 23; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
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Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 10
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```

US-09-853-731-1
; Sequence 1, Application US/09853731
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 23; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 11
US-09-854-018-1
; Sequence 1, Application US/09854018
; GENERAL INFORMATION:
; APPLICANT: Herberger, John
; TITLE OF INVENTION: Secondary Drying of Microparticles Using Pressurized Carbon Dioxi
; FILE REFERENCE: A-786
; CURRENT APPLICATION NUMBER: US/09/854,018
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Human
US-09-854-018-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 23; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 12
US-09-945-517-1
; Sequence 1, Application US/09945517
; GENERAL INFORMATION:
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APPLICANT: Li, Tiansheng
APPLICANT: Chang, Byeong
APPLICANT: Sloey, Christopher
TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
FILE REFERENCE: A-803
CURRENT APPLICATION NUMBER: US/09/945,517
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.0
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-945-517-1
Query Match 100.0%; Score 846; DB 24; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
RESULT 13
US-10-014-363-1
Sequence 1, Application US/10014363
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-363-1
Query Match 100.0%; Score 846; DB 26; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
RESULT 14

US-10-241-356-1
Sequence 1, Application US/10241356
GENERAL INFORMATION:
APPLICANT: Tischer, Wilhelm
TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
FILE REFERENCE: 20971
CURRENT APPLICATION NUMBER: US/10/241,356
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: EP 01122555.4
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-10-241-356-1
Query Match 100.0%; Score 846; DB 28; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
RESULT 15
US-10-293-551-1
Sequence 1, Application US/10293551
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/293,551
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/604,938
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-551-1
Query Match 100.0%; Score 846; DB 28; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLETTITADTFERKLFVYSNPLRGKUKLYTGEACRTGD 165
DB 121 PPDAASAAPLETTITADTFERKLFVYSNPLRGKUKLYTGEACRTGD 165

Search completed: May 25, 2004, 11:27:23
Job time : 185 secs

result No.	Score	Query		DB	ID	Description
		Match	\$			
1	846	100.0	165	1	PCT-US04-11494-73	Sequence 73, Appl
2	846	100.0	165	6	US-10-634-477-1	Sequence 1, Appl
3	846	100.0	165	6	US-10-780-287-1	Sequence 1, Appl
4	846	100.0	166	6	US-10-780-287-2	Sequence 2, Appl
5	846	100.0	166	6	US-10-658-834A-201	Sequence 201, App
6	846	100.0	166	6	US-10-773-939-2	Sequence 2, Appl
7	846	100.0	166	6	US-10-774-149-2	Sequence 2, Appl
8	846	100.0	192	6	US-10-775-204-593	Sequence 593, App
9	846	100.0	192	6	US-10-775-204-594	Sequence 594, App
10	846	100.0	192	6	US-10-775-204-603	Sequence 603, App
11	846	100.0	192	6	US-10-775-204-1689	Sequence 1689, Ap
12	846	100.0	192	6	US-10-775-204-1690	Sequence 1690, Ap
13	846	100.0	192	6	US-10-775-204-1691	Sequence 1691, Ap
14	846	100.0	192	6	US-10-775-204-1828	Sequence 1828, Ap
15	846	100.0	192	6	US-10-775-204-1829	Sequence 1829, Ap
16	846	100.0	192	6	US-10-775-204-1830	Sequence 1830, Ap
17	846	100.0	193	1	PCT-US04-10353-3	Sequence 3, Appl
18	846	100.0	193	1	PCT-US04-10353-9	Sequence 9, Appl
19	846	100.0	193	1	PCT-US04-13099-10	Sequence 10, Appl
20	846	100.0	193	1	PCT-US04-13099-22	Sequence 22, Appl
21	846	100.0	193	1	PCT-US04-13099-112	Sequence 112, App
22	846	100.0	435	6	US-10-761-593A-22	Sequence 22, Appl
23	846	100.0	436	6	US-10-761-593A-18	Sequence 18, Appl
24	846	100.0	437	6	US-10-761-593A-20	Sequence 20, Appl
25	846	100.0	768	6	US-10-775-204-1521	Sequence 1521, Ap
26	846	100.0	768	6	US-10-775-204-1522	Sequence 1522, Ap

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QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 2
US-10-634-477-1
; Sequence 1, Application US/10634477
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Paul
; APPLICANT: Roediger, Ralf
; APPLICANT: Walter-Matsui, Ruth
; TITLE OF INVENTION: TREATMENT OF DISTURBANCES OF IRON DISTRIBUTION
; FILE REFERENCE: 21368
; CURRENT APPLICATION NUMBER: US/10/634,477
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 02019100.3
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-634-477-1

Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 3
US-10-780-297-1
; Sequence 1, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-1

Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 4
US-10-780-297-2
; Sequence 2, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 5
US-10-658-834A-201
; Sequence 201, Application US/10658834A
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Driettanci, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
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Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 4
US-10-780-297-2
; Sequence 2, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLLKLYTGEACRTGD 165

RESULT 5
US-10-658-834A-201
; Sequence 201, Application US/10658834A
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Driettanci, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 201
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAAS2400
DATABASE ENTRY DATE: 1994-11-08
S-10-658-834A-201

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 6

US-10-773-939-2
Sequence 2, Application US/10773939
GENERAL INFORMATION:
APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10773,939
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2
LENGTH: 166
TYPE: PRT

ORGANISM: Homo sapiens
US-10-773-939-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 7

US-10-774-149-2
Sequence 2, Application US/10774149
GENERAL INFORMATION:
APPLICANT: Cox III, George N

APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/774,149
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-774-149-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRSLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 8

US-10-775-204-593
Sequence 593, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.

TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 593
LENGTH: 192

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-594

Query Match      100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 147

QY 121 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 192

RESULT 9
US-10-775-204-594
; Sequence 594, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS64
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 594
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-594

Query Match      100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 147

QY 121 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 192

RESULT 10
US-10-775-204-603
; Sequence 603, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS64
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 603
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-603

Query Match      100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKAEENITTCABHCNSLNENITVPDTKKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 147

QY 121 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTRFKLFRVYSNFRGLKGLKLYTGEACRTGD 192

RESULT 11
US-10-775-204-1689
; Sequence 1689, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
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FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1689
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1690

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 APPLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPTKVNFWAKMEVGGQA 60
2b 28 APPLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPTKVNFWAKMEVGGQA 87
2y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
2b 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 147
2y 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
2b 148 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 12
US-10-775-204-1690
Sequence 1690, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1691
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens

PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1690
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1690

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPTKVNFWAKMEVGGQA 60
Db 28 APPLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPTKVNFWAKMEVGGQA 87
Qy 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 147
Qy 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 13
US-10-775-204-1691
Sequence 1691, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1691
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens

US-10-775-204-1691

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 14

US-10-775-204-1828
; Sequence 1828, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1828
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1828

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165

Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 15
US-10-775-204-1829
; Sequence 1829, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1829
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1829

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

Search completed: May 25, 2004, 11:27:56
Job time : 21 secs

GenCore version 5.1.6
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JM protein - protein search, using sw model

run on: May 25, 2004, 11:15:48 ; Search time 18 seconds

(without alignments)
477,310 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APRLLICDSRVLYLEAK.....SNFLRGKLYTGEACRTGD 165

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Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	759.5	89.8	192	1	EPO_NACMU
4	706	83.5	192	1	EPO_FELCA
5	701	82.9	192	1	EPO_RAT
6	692.5	81.9	192	1	EPO_BOVIN
7	689	81.4	192	1	EPO_MOUSE
8	685.5	80.1	194	1	EPO_SHEEP
9	678	80.1	190	1	EPO_PIG
10	638	75.4	175	1	EPO_CANFA
11	109	12.9	352	1	TPO_CANFA
12	89	10.5	353	1	TPO_HUMAN
13	83	9.8	339	1	MURB_PSEAB
14	82	9.7	548	1	CH60_BUCPP
15	80.5	9.5	3033	1	POLG_HCVU8
16	78.5	9.3	897	1	EP15_MOUSE
17	78	9.2	548	1	CH60_BUCAP
18	78	9.2	548	1	CH60_BUCRM
19	78	9.2	747	1	ATCS_SYN7
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21	76.5	9.0	386	1	CTBP_DROME
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23	75	8.9	545	1	CH60_SHEON
24	75	8.9	548	1	CH60_BUCRP
25	74.5	8.8	552	1	CH60_PSEST
26	74.5	8.8	809	1	HRBB_ECOLI
27	74	8.7	326	1	TPO_RAT
28	74	8.7	551	1	CH60_BUCCM
29	74	8.7	1564	1	PDRA_YEAST
30	73.5	8.7	830	1	GCL2_MOUSE
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32	73	8.6	283	1	YH25_DEIRA
33	73	8.6	1089	1	IMB3_YEAST

RESULT 1

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DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	EPO.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.,			
RA	Murson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.;			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloekner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes.";			
RT	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rupert J.L., Hochachka P.W.;			
RA	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	Population.";			
RT	Submitted (NOV-1999) to the ENBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHE-132 AND GLN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RA	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RT	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			
RP	SEQUENCE OF 28-193, AND DISULFIDE BONDS.			
RP	TISSUE=Urine;			

ALIGNMENTS

34	72.5	8.6	762	1	SLAP_ACEKI
35	72	8.5	356	1	TPO_MOUSE
36	72	8.5	548	1	CH60_BUCAI
37	71	8.4	333	1	YF72_HALN1
38	70.5	8.3	217	1	YNJD_ECOLI
39	70.5	8.3	381	1	APA_MCANV
40	70.5	8.3	543	1	CH60_BARBA
41	70.5	8.3	896	1	EP15_HUMAN
42	70	8.3	319	1	RIR4_SALTY
43	70	8.3	475	1	Z342_HUMAN
44	70	8.3	547	1	CH60_LEGPN
45	70	8.3	550	1	CH60_BUCBP
					P22258 acetogenium
					P40226 mus musculus
					P25750 buchnera ap
					Q9hpl8 halobacteri
					P76909 escherichia
					Q48919 mycobacteri
					P35635 bartonella
					P43566 homo sapien
					P17424 salmonella
					Q8wu44 homo sapien
					P26878 legionella
					P59522 buchnera ap

P22258	acetogenium
P40226	mus musculus
P25750	buchnera ap
Q9hpl8	halobacteri
P76909	escherichia
Q48919	mycobacteri
P35635	bartonella
P42566	homo sapien
P17424	salmonella
Q8wu4	homo sapien
P26878	legionella
P59526	buchnera ap

2Y	61	VEVWGGLALISEAVLRGCAALLVNSSQWPEIQLHVDKAVSGLSLSITLLRALCAQKEAIS	120
2B	88	VEVWGGLALLSEAVLRGCAALLVNSSQWPEIQLHVDKAVSGLSLSITLLRALCAQKEAIS	147
2Y	121	PPDAASAAPLTIITADTFKRLFRVYSNFLRGKLYTGEACRTGD	165
2B	148	PPDAASAAPLTIITADTFKRLFRVYSNFLRGKLYTGEACRTGD	192

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RESULT 2
INFO_MACFA
ID EPO_MACFA STANDARD; PRT; 192 AA.
CC P07865;
CC 01-AUG-1988 (Rel. 08, Created)
CC 01-AUG-1988 (Rel. 08, Last sequence update)
CC 16-OCT-2001 (Rel. 40, Last annotation update)
CC Erythropoietin precursor.
CC EPO.
CC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecinae; Macaca.
CC NCBI_TaxID=9541;
CC [1]
CC IN SEQUENCE FROM N.A.
CC IP MEDLINE=87055236; PubMed=2877922;
CC RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
CC RA Fox G.M., Chen K.K., Castro M., Suggs S.;
CC RT "Monkey erythropoietin gene: cloning, expression and comparison with
CC RT the human erythropoietin gene.";
CC RL Gene 44:201-209(1986).
CC
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
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IC	EMBL; M18189; AAA36841.1; -	
DR	PIR; JQ0173; JQ0173.	
DR	HSSP; F01588; 1CN4.	
DR	InterPro; IPR001323; EPO_TPO.	
DR	InterPro; IPR003013; EryEhroptn.	
DR	Pfam; PF00759; EPO_TPO.1	
DR	PRINTS; PR00272; ERYTHROPTN.	
DR	PROSITE; PS00817; EPO_TPO; 1.	
KW	Erythrocyte maturation; Glycoprotein; Hormone; Signal.	
FT	SIGNAL	1 27
FT	CHAIN	28 192
FT	DISULFID	34 187
FT	DISULFID	56 60
FT	CARBOHYD	51 51
FT	CARBOHYD	65 65
FT	CARBOHYD	110 110
FT	CARBOHYD	152 152
FT	SEQUENCE	192 AA; 21113 MW; E8A900FA42AD4522 CRG664;
EQ		

Query Match 90.4%; Score 764.5; DB 1; Length 192;
Best Local Similarity 91.5%; Pred. No. 4.1e-66;
Matches 151; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

2y 1 APPRLCDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNIFYAWKRMVEVGQQA 60

Db	28	APRPLICDSRVLRYLEAKAEAEVNTWCSSCSLNENITVPDTKNFYAWKEMEVGGQA	87
Qy	61	VEVWGQALLSEAVLRGQALLVNSQSWEPEQLHVDKAVSGLRSLTITLLRALGAQAEAS	120
Db	88	VEVWGQALLSEAVLRGQAVLANSQPEPEQLHMDKAIISGLRSITITLLRALGAQ-EAIS	146
Qy	121	PDAAASAAPLTITADTPKLFVYSNFRGKGLYTGECRTGD	165
Db	147	LPDAAASAAPLTITADTECKLFVYSNFRGKGLYTGECRGGD	191

RESULT 3

EPO	MACMU	STANDARD;	PRT;	192 AA.
ID	EFO			
AC	Q28513;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Erythropoietin precursor.			
GN	EFO.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_Taxid=95544;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Kidney;			
RX	MEDLINE=933732347; PubMed=8364201;			
RA	Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,			
RA	Czelusniak J., Goodman M., Bunn H.F.;			
RT	"Erythropoietin structure-function relationships: high degree of			
RT	sequence homology among mammals.";			
RL	Blood 82:1507-1516(1993).			
CC	-1- FUNCTION: Erythropoietin is the principal hormone involved in the			
CC	regulation of erythrocyte differentiation and the maintenance of a			
CC	physiological level of circulating erythrocyte mass.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals			
CC	and by liver of fetal or neonatal mammals.			
CC	-1- SIMILARITY: Belongs to the EPO / TPO family.			
CC				
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CC	or send an email to license@isb-sib.ch).			

CC	ENBL; L10609; ARA36842.1; -.				
DR	FXB; I84613; I84613.				
DR	HSPF; P01586; ICM4.				
DR	InterPro; IPR001323; EPO TPO.				
DR	InterPro; IPR003013; EryThroptn.				
DR	Pfam; PF00758; EPO TPO; 1.				
DR	PRINTS; PR00272; ERYTHROPTN.				
DR	PROSITE; PS00817; EPO TPO; 1.				
KM	Erythrocyte maturation; Glycoprotein; Hormone; Signal.				
FT	SIGNAL	1	27	BY SIMILARITY.	
FT	CHAIN	28	192	ERYTHROPOIETIN.	
FT	DISULFID	34	187	BY SIMILARITY.	
FT	DISULFID	56	60	BY SIMILARITY.	
FT	CARBOHYD	51	51	N-LINKED (GLCNAC. . .)	(BY SIMILARITY).
FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .)	(BY SIMILARITY).
FT	CARBOHYD	110	110	N-LINKED (GLCNAC. . .)	(BY SIMILARITY).
FT	CARBOHYD	152	152	O-LINKED (GALNAC. . .)	(BY SIMILARITY).
FO	SEQUENCE	192 AA;	21681 MW;	275560A264628CD1	CRC664;

Query Match	89.8%;	Score 759.5;	DB 1;	Length 192;
Best Local Similarity	90.3%;	Pred. No. 1.2e-65;		
Matches 149;	Conservative	9;	Mismatches 6;	Indels 1;
				Gaps 1;

```
QY 1 APPRLICDSRVLYRLEAKAEANITGCAEHCSLNENITVPDTKYNFYAKMEVGGQA 60
DB 28 APPRLVCDSDRVLYRLEAKAEANITGCAEHCSLNENITVPDTKYNFYAKMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRACGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRACGAQKEAIS 146
QY 121 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
DB 147 LPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 191

RESULT 4
EPO_FELCA
ID EPO_FELCA STANDARD; PRT; 192 AA.
AC P33708;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-192 FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC and by liver of fetal or neonatal mammals.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; U00685; AAA18282.1; -.
CC ENBL; L10606; AAA30807.1; -.
CC PIR; I46083; I46083.
CC HSSP; P01588; 1CN4.
CC InterPro; IPR001323; EPO TPO.
CC Pfam; PF00758; EPO TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
KW SIGNAL
FT CHAIN 1 26 BY SIMILARITY.
FT FT 27 192 ERYTHROPOIETIN.
FT FT 33 187 BY SIMILARITY.
FT FT 35 59 BY SIMILARITY.
FT FT 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT 44 44 G -> E (IN REF. 2).
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QY 1 APPRLICDSRVLYRLEAKAEANITGCAEHCSLNENITVPDTKYNFYAKMEVGGQA 60
DB 27 APPRLVCDSDRVLYRLEAKAEANITGCAEHCSLNENITVPDTKYNFYAKMEVGGQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRACGAQKEAIS 120
DB 87 VEVWQGLALLSEAVLRGQALLVNSQPSETLQLHVDKAVSSLSRLTLLRACGAQKEAIS 146
QY 121 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
DB 147 LPEATSAAPLRTFTVDTLCKLFRIYSNFRGLKLYTGEACRTGD 191

RESULT 5
EPO_RAT
ID EPO_RAT STANDARD; PRT; 192 AA.
AC P29576; P70504;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WiStar; TISSUE=Kidney;
RX MEDLINE=93042015; PubMed=420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Sasaki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
RN [2]
RP SEQUENCE OF 4-192 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
RA Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC
CC ENBL; D10763; BAA01593.1; -.
CC ENBL; L10608; AAA41126.1; -.
CC PIR; S28148; S28148.
CC HSSP; P01588; 1CN4.
CC InterPro; IPR001323; EPO TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC
```

DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 27 192 ERYTHROPOIETIN.
FT DISULFID 33 187 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
Q SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;
Query Match 82.9%; Score 701; DB 1; Length 192;
Best Local Similarity 82.4%; Pred. No. 5e-60;
Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
Y 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
b 27 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVQA 86
Y 61 VEVQGLALLSEAVLRQALLVNSQWPEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
b 87 VEVQGLALLSEAVLRQALLVNSQWPEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 146
Y 121 PDAAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGD 165
b 147 PDATQAPLRTITADTFKLFVYNSFLRGKLYTGACRTGD 191
RESULT 6
PO BOVIN
D EPO BOVIN STANDARD; PRT; 192 AA.
AC P45617;
Y 01-FEB-1996 (Rel. 33, Created)
Y 01-FEB-1996 (Rel. 33, Last sequence update)
Y 16-OCT-2001 (Rel. 40, Last annotation update)
Y Erythropoietin precursor.
N EPO.
N Bos taurus (Bovine).
N Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
N Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
N Bovidae; Bovinae; Bos.
N NCBI_TaxID=9913;
N (1)
N SEQUENCE FROM N.A.
N STRAIN=Boran; TISSUE=Kidney;
N MEDLINE=96257233; PubMed=9666286;
N Suliman H.B., Majiwa P.A.O., Feldman B.F., Mertens B.,
N Logan-Henfrey L.B.;
N "Cloning of a cDNA encoding bovine erythropoietin and analysis of its
N transcription in selected tissues.";
N Gene 171:275-280(1996).
N -!- FUNCTION: Erythropoietin is the principal hormone involved in the
N regulation of erythrocyte differentiation and the maintenance of a
N physiological level of circulating erythrocyte mass.
N -!- SUBCELLULAR LOCATION: Secreted.
N -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
N and by liver of fetal or neonatal mammals.
N -!- SIMILARITY: Belongs to the EPO / TPO family.
N -----
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N -----
N EMBL; L41354; AAB41268.1; -;
N EMBL; U44762; AAB46653.1; -;
N HSSP; P01568; 1CN4.
N InterPro; IPR001323; EPO_TPO.
N InterPro; IPR003013; Erythroptn.
N Pfam; PF00758; EPO_TPO; 1.
N PRINTS; PR00272; ERYTHROPTN.

DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 27 192 ERYTHROPOIETIN.
FT DISULFID 33 187 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
Q SEQUENCE 192 AA; 21075 MW; DBC419022F7B483A CRC64;
Query Match 81.9%; Score 692.5; DB 1; Length 192;
Best Local Similarity 83.1%; Pred. No. 3.3e-59;
Matches 138; Conservative 8; Mismatches 19; Indels 1; Gaps 1;
Y 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 60
b 26 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMVEVGQA 85
Y 61 VEVQGLALLSEAVLRQALLVNSQWPEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
b 86 LEVQGLALLSEAVLRQALLVNSQWPEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 145
Y 121 PDAAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGD 165
b 146 LPDAPLRTITADTFKLFVYNSFLRGKLYTGACRTGD 191
RESULT 7
EPO MOUSE
ID EPO MOUSE STANDARD; PRT; 192 AA.
AC P07321;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=87039105; PubMed=3773894;
RX Shoemaker C.B., Mitscock L.D.;
RT "Murine erythropoietin gene: cloning, expression, and human gene
RT homology.";
RL Mol. Cell. Biol. 6:849-858(1986).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=87039104; PubMed=3022133;
RX McDonald J.D., Lin F.-K., Goldwasser E.;
RT "Cloning, sequencing, and evolutionary analysis of the mouse
RT erythropoietin gene.";
RL Mol. Cell. Biol. 6:842-848(1986).
RN (3)
RN SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RX Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RX Cheng T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RX Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense Ache/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365(2001).
RN (4)
RN SEQUENCE OF 1-52 FROM N.A.
RP STRAIN=1CFW;
RX MEDLINE=98030528; PubMed=9365246;
RX Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
RX Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IW32 cells results from a rearrangement between the

RT G- protein beta2 subunit gene and the Epo gene.;"

RL Oncogene 15:1995-1999(1997);

CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the

CC regulation of erythrocyte differentiation and the maintenance of a

CC physiological level of circulating erythrocyte mass.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals

CC and by liver of fetal or neonatal mammals.

CC -!- SIMILARITY: Belongs to the EPO / TPO family.

CC

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CC

DR EMBL; M12482; AAA37568.1; -

DR EMBL; M12930; AAA37570.1; -

DR EMBL; AF312033; AAK28825.1; -

DR EMBL; Y11971; CAA72707.1; -

DR PIR; A24902; A24902.

DR HSSP; P01588; 1CM4.

DR MGD; MGI:95407; Epo.

DR InterPro; IPR001323; EPO TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

DR PROSITE; PS00817; EPO TPO; 1.

KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 26

FT CHAIN 27 192 ERYTHROPOIETIN.

FT BY SIMILARITY.

FT DISULFID 33 187

FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (BY SIMILARITY).

FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (BY SIMILARITY).

FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (BY SIMILARITY).

SQ SEQUENCE 192 AA; 21365 MW; 65F942E14E0DF2E CRC64;

Query Match 81.4%; Score 689; DB 1; Length 192;

Best Local Similarity 80.0%; Pred. No. 7.1e-59;

Matches 132; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 60

Db 27 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVEEQA 86

QY 61 VEYVQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQKAIS 120

Db 87 IEVWQGLSLSEAILQALLANSOPPBTLLQHLIDKKAISGLSLTSLRLVLGAKQKELMS 146

QY 121 PPDAAAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGD 165

Db 147 PPDTPPAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGD 191

RESULT 8

EPO_SHEEP STANDARD; PRT; 194 AA.

AC P33709; Q28572;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

GN Erythropoietin precursor.

DE EPO.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=93351736; PubMed=8349021;

RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;

RT "The sheep erythropoietin gene: molecular cloning and effect of

RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in

RT adult sheep.;"

RL Mol. Cell. Endocrinol. 93:107-116(1993).

RN [2]

RP SEQUENCE OF 4-194 FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=93372347; PubMed=8364201;

RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RA Czelusniak J., Goodman M., Bunn H.F.;

RT "Erythropoietin structure-function relationships: high degree of

RT sequence homology among mammals.;"

RL Blood 82:1507-1516(1993).

CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the

CC regulation of erythrocyte differentiation and the maintenance of a

CC physiological level of circulating erythrocyte mass.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals

CC and by liver of fetal or neonatal mammals.

CC -!- SIMILARITY: Belongs to the EPO / TPO family.

CC

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CC

DR EMBL; Z24681; CAA80848.1; -

DR EMBL; L10610; AAA31518.1; -

DR PIR; I46401; I46401.

DR HSSP; P01588; 1CM4.

DR InterPro; IPR001323; EPO TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

DR PROSITE; PS00817; EPO TPO; 1.

KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 27

FT CHAIN 28 194 ERYTHROPOIETIN.

FT BY SIMILARITY.

FT DISULFID 34 189

FT DISULFID 56 60 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 110 110 F -> L (IN REF. 2).

FT CONFLICT 16 16

FT CONFLICT 108 108 L -> P (IN REF. 2).

SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;

Query Match 81.0%; Score 685.5; DB 1; Length 194;

Best Local Similarity 81.9%; Pred. No. 1.6e-58;

Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 60

Db 28 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 87

QY 61 VEYVQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQKAIS 120

Db 88 LEVWQGLALLSEAFRGQALLANSQPCEALRHVDKAVSGLSRLTLLRALGAKQKAIP 147

QY 121 PPDAA- SAAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGD 165

Db 148 LPDATPSAAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGD 193

RESULT 9

EPO_PIG STANDARD; PRT; 190 AA.

ID -EPO_PIG

AC P49157;

01-FEB-1996 (Rel. 33, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Erythropoietin precursor (Fragment).
 EPO.
 Sus scrofa (Pig).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 [1]
 C TISSUE=Kidney;
 P SEQUENCE FROM N.A.
 X MEDLINE=93372347; PubMed=8364201;
 A Wen D., Boiesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 Czelusniak J., Goodman M., Bunn H.F.;
 T "Erythropoietin structure-function relationships: high degree of
 T sequence homology among mammals.";
 L Blood 82:1507-1516(1993)
 C -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 C regulation of erythrocyte differentiation and the maintenance of a
 C physiological level of circulating erythrocyte mass.
 C -!- SUBCELLULAR LOCATION: Secreted.
 C -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 C and by liver of fetal or neonatal mammals.
 C -!- SIMILARITY: Belongs to the EPO / TPO family.
 C
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 C or send an email to license@isb-sib.ch).
 C
 C EMBL; L10607; AAA31029.1; -;
 C PIR; I46578; I46578.
 C HSSP; P01588; 1CN4.
 C InterPro; IPR001323; EPO.TPO.
 C InterPro; IPR003013; Erythroptn.
 C Pfam; PF00758; EPO.TPO; 1.
 C PRINTS; PR00272; ERYTHROPTN.
 C PROSITE; PS00817; EPO.TPO; 1.
 C Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 C
 C NON TER 1 1
 C SIGNAL <1 22 POTENTIAL.
 C CHAIN 23 190 ERYTHROPOIETIN.
 C BY SIMILARITY.
 C DISULFID 29 185 BY SIMILARITY.
 C DISULFID 51 55 BY SIMILARITY.
 C CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;
 C
 C Query Match 80.1%; Score 678; DB 1; Length 190;
 C Best Local Similarity 82.0%; Pred. No. 7.9e-58;
 C Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
 C
 C 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCHSLNENITVPDTKNFYAKRMEVQQA 60
 C 23 APPRLICDSRVLELYLLEAKEAENITTCGAHCHSLNENITVPDTKNFYAKRMEVQQA 82
 C
 C 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 C 83 MEVWQGLALLSEALIQGALLANSQSPSEALQLHVDKAVSGLSRLTLLRALGAQKEAIP 142
 C
 C 121 PPDA--ASAPLRTITADTFKLFVYNSFLRGKLYTGACHTGD 165
 C 143 LPDASPSATPRTFAVDTLCKLFRVNSFLRGKLYTGACRRD 189

RESULT 10
 EPO_CANFA

ID EPO_CANFA STANDARD; PRT; 175 AA.
 AC P33707;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor (Fragment).
 DE EPO.
 GN Canis familiaris (Dog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boiesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 C -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 C regulation of erythrocyte differentiation and the maintenance of a
 C physiological level of circulating erythrocyte mass.
 C -!- SUBCELLULAR LOCATION: Secreted.
 C -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 C and by liver of fetal or neonatal mammals.
 C -!- SIMILARITY: Belongs to the EPO / TPO family.
 C
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 C or send an email to license@isb-sib.ch).
 C
 C EMBL; L13027; AAA30842.1; -;
 C PIR; I46199; I46199.
 C HSSP; P01588; 1CN4.
 C InterPro; IPR001323; EPO.TPO.
 C InterPro; IPR003013; Erythroptn.
 C Pfam; PF00758; EPO.TPO; 1.
 C PRINTS; PR00272; ERYTHROPTN.
 C PROSITE; PS00817; EPO.TPO; 1.
 C Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 C
 C NON TER 1 1
 C SIGNAL <1 22 BY SIMILARITY.
 C CHAIN 23 >175 ERYTHROPOIETIN.
 C BY SIMILARITY.
 C DISULFID 29 >175 BY SIMILARITY.
 C DISULFID 51 55 BY SIMILARITY.
 C CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C NON TER 175 175
 C SEQUENCE 175 AA; 19193 MW; B504F8DE86676BF4 CRC64;
 C
 C Query Match 75.4%; Score 638; DB 1; Length 175;
 C Best Local Similarity 81.0%; Pred. No. 4.9e-54;
 C Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 C
 C 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCHSLNENITVPDTKNFYAKRMEVQQA 60
 C 23 APPRLICDSRVLELYLLEAKEAENITTCGAHCHSLNENITVPDTKNFYAKRMEVQQA 82
 C
 C 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 C 83 LEVWQGLALLSEALIRGALLANASQSPETPQLHVDKAVSSLSRLTLLRALGAQKEAIS 142
 C
 C 121 PPDAASAPLRTITADTFKLFVYNSFLRGKLYTGACHTGD 153
 C 143 LPDASAPLRTITADTFKLFVYNSFLRGKLYTGACHTGD 175

RESULT 11

TPO_CANFA ID TPO_CANFA STANDARD; PRT; 352 AA.
AC P42705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
DE (C-MPL ligand) (ML) (Megakaryocyte growth and development factor)
DE (MGDF)
GN THPO OR TPO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.
RC TISSUE=Kidney;
RX MEDLINE=94291201; PubMed=8020099;
RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellinan M.,
Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
Shuter J., Chute H., Basu R., Selander L., Trollinger D., Sieu L.,
Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
Pacifici R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
Bosselman R.A.;
RP "Identification and cloning of a megakaryocyte growth and development
factor that is a ligand for the cytokine receptor Mpl.";
RL Cell 77:1117-1117(1994).
CC -!- FUNCTION: Lineage-specific cytokine affecting the proliferation
and maturation of megakaryocytes from their committed progenitor
cells. It acts at a late stage of megakaryocyte development. It
may be the major physiological regulator of circulating platelets.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: Two-domain structure with an erythropoietin-like N-
terminal and a Ser/Pro/Thr-rich C-terminal.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR01485; THROMBOPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Cytokine; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 23
FT CHAIN 24 352 THROMBOPOIETIN.
FT DISULFID 28 172 POTENTIAL.
FT DISULFID 50 106 POTENTIAL.
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 352 AA; 37641 MW; 024F3B41B061FED8 CRC64;
Query Match 12.9%; Score 109; DB 1; Length 352;
Best Local Similarity 24.0%; Pred. No. 0.0054;
Matches 40; Conservative 23; Mismatches 62; Indels 42; Gaps 5;
QY 1 APPRLTCDSRVLYLEAKEAENITTCBAEHCNSLNENITVPTKVFYAMKMEVGQQA 60
DB 24 APP-ACDPELLNKMRLDSHVLSRLSCPDYPLSTFTVLLPAVDVDFSLGKWTKEQTKA 81
QY 61 VEVWQGLALISAVL--RQALVNSQWPEPLQHVDKVAGSLRSITLTLRALCAQKEA 118
DB 82 QDWGAVALLDGVLAARQQL-----GPSCLSSLLGQLSGQVRL 120
QY 119 I-----SPDPAASAPLRTITADTFKFLPRVYSNFLRGK 154
DB 121 LIGALQQLIGTQLPFG-----RTTHKDPNAIFLSFQQLRGKVR 161

RESULT 12
TPO_HUMAN ID TPO_HUMAN STANDARD; PRT; 353 AA.
AC P40225; Q13020; Q15790; Q15791; Q15792;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
DE (Myeloproliferative leukemia virus oncogene ligand) (C-mpl ligand)
DE (ML) (Megakaryocyte growth and development factor) (MGDF).
GN THPO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal liver;
RX MEDLINE=94261202; PubMed=8202154;
RA de Sauvage F.J., Haas P.E., Spencer S.D., Malloy B.E., Gurney A.L.,
Spencer S.A., Darbonne W.C., Henzel W.J., Wong S.C., Kuang W.-J.,
Oles K.J., Hultgren B., Solberg L.A. Jr., Gosdel D.V., Eaton D.L.,
"Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl
ligand.";
RL Nature 369:533-538(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal liver;
RX MEDLINE=94291201; PubMed=8020099;
RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellinan M.,
Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
Shuter J., Chute H., Basu R., Selander L., Trollinger D., Sieu L.,
Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
Pacifici R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
Bosselman R.A.;
RP "Identification and cloning of a megakaryocyte growth and development
factor that is a ligand for the cytokine receptor Mpl.";
RL Cell 77:1117-1124(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95108091; PubMed=7809166;
RA Foster D.C., Spracher C.A., Grant F.J., Kramer J.M., Kuijper J.L.,
Holly R.D., Whitmore T.E., Heipel M.D., Bell L.A.N., Ching A.F.,
McGrane V., Hart C., O'Hara P.J., Lok S.;
"Human thrombopoietin: gene structure, cDNA sequence, expression, and
chromosomal localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:13023-13027(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95010765; PubMed=7926023;
RA Sohna Y., Akahori H., Seki N., Hori T.-A., Ogami K., Kawamura K.,
Miyazaki H.;
"Molecular cloning and chromosomal localization of the human
thrombopoietin gene.";
RL FEBS Lett. 353:57-61(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=95152076; PubMed=7849319;
RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L.,
de Sauvage F.J.;
"Genomic structure, chromosomal localization, and conserved
alternative splice forms of thrombopoietin.";
RL Blood 85:981-988(1995).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=96015174; PubMed=8537317;

KA Kato T., Ogami K., Shimada Y., Iwamatsu A., Sohna Y., Akahori H.,
KA Horie K., Kokubo A., Kudo Y., Maeda E., Kobayashi K., Ohashi H.,
KA Ozawa T., Inoue H., Kawamura K., Miyazaki H.,
IT "Purification and characterization of thrombopoietin.";
J. Biochem. 118:229-236(1995).
[7]
IN SEQUENCE FROM N.A. (ISOFORM 1).
IC TISSUE=Placenta;
X MEDLINE=9512248; PubMed=7822271;
A Chang M., McNinch J., Basu R., Shutter J., Heu R., Perkins C., Mar V.,
A Suggs S., Welcher A., Li L., Lu H., Bartley T., Hunt P., Martin F.,
A Samal B., Bogenberger J.,
IT "Cloning and characterization of the human megakaryocyte growth and
development factor (MGDF) gene.";
J. Biol. Chem. 270:511-514(1995).
[8]
IN SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
A Im S.H., Lee W.S., Chung K.H.;
IT "Cloning and sequencing of human thrombopoietin.";
Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
L -!- FUNCTION: Lineage-specific cytokine affecting the proliferation
and maturation of megakaryocytes from their committed progenitor
cells. It acts at a late stage of megakaryocyte development. It
may be the major physiological regulator of circulating platelets.
C -!- SUBCELLULAR LOCATION: Secreted.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=3;
C Name=1;
C IsoId=P40225-1; Sequence=displayed;
C Name=2; Synonyms=TPO-2;
C IsoId=P40225-2; Sequence=VSP_001450;
C Name=3; Synonyms=Truncated;
C IsoId=P40225-3; Sequence=VSP_001451;
C -!- DOMAIN: Two-domain structure with an erythropoietin-like N-
terminal and a Ser/Pro/Thr-rich C-terminal.
C -!- SIMILARITY: Belongs to the EPO / TPO family.
C -!- DATABASE: NAME=R&D Systems' cytokine source book: TPO;
C WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=225".
C
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or send an email to license@isb-sib.ch).
C
C -----
C EMBL; L33410; AAA59857.1; -
C EMBL; U11025; AAA50553.1; -
C EMBL; L36051; AAC37568.1; -
C EMBL; L36052; AAC37566.1; -
C EMBL; D32046; BAA06807.1; -
C EMBL; S76771; AAB33390.1; -
C EMBL; D32047; BAA21930.1; -
C EMBL; U59493; AAB03392.1; -
C EMBL; U59494; AAB03393.1; -
C EMBL; U59495; AAB03394.1; -
C EMBL; U17071; AAX74083.1; -
C F1R; I59281; I80105.
C Genew; HGNC:11795; THPO.
C MIM; 600044; -
C GO; GO:0008083; P:cell growth factor activity; TAS.
C GO; GO:0008283; P:cell proliferation; TAS.
C GO; GO:0007275; P:development; TAS.
C InterPro; IPR001323; EPO_TPO.
C InterPro; IPR003978; thrombopoietin.
C Pfam; PF00758; EPO_TPO; 1.
C PRINTS; PR01485; THROMOPTN.
C PROSITE; PS00817; EPO_TPO; 1.
C Cytokine; Glycoprotein; Hormone; Signal; Alternative splicing;
C Polymorphism. 1 21 POTENTIAL.
C SIGNAL 22 353 THROMBOPOIETIN.
C CHAIN

FT DISULFID 28 172 POTENTIAL.
FT DISULFID 50 106 POTENTIAL.
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 133 136 Missing (in isoform 2).
FT VARSPLIC 160 198 /FTID=VSP_001450.
FT VARSPLIC 160 198 Missing (in isoform 3).
FT VARIANT 14 14 /FTID=VSP_001451.
FT VARIANT 116 116 L -> P (in dbSNP:1042346).
FT VARIANT 116 116 G -> E (in dbSNP:1126665).
FT CONFLICT 46 46 R -> K (in REF. 8).
FT CONFLICT 76 76 M -> MSQ (in REF. 7).
FT CONFLICT 113 113 Q -> E (in REF. 2).
FT CONFLICT 131 131 T -> P (in REF. 7).
FT CONFLICT 277 277 G -> E (in REF. 8; AAB03393/AAB03394).
FT CONFLICT 346 346 S -> C (in REF. 8; AAB03393/AAB03394).
SQ SEQUENCE 353 AA; 37822 MW; F0AB5449B7E5526 CRC64;
Query Match 10.5%; Score 89; DB 1; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.45;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;
QY 1 APRLLCDSRVLEKAEENITTCARHCSENENITVDTKVNFAVKRMEVGQQA 60
DB 24 APP--ACDLRVLSKLRDSHVLSQCPVHPPTVLLPAVDVDFSLGKMTQWETKA 81
QY 61 VEYVQGLALISEAVL--RQALLVNSQWPQLQLHVDKAVSGLSRLTLTLALGAQKEA 118
DB 82 QDILGAVTLLEGVMAARGQLGPTCLSLGLQSLGQVRLLLGALQSL-----LGTQ--- 132
QY 119 ISPPDAASAPRTITADTFKLFVRYNSFLRGKLLK 154
DB 133 -LPPOG-----RTTAHKDPNNAIF-SFQHLRGRVR 161
RESULT 13
MURB_PSEAE
ID_MURB_PSEAE STANDARD; PRT; 339 AA.
AC Q9H2M7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylglucosaminylglucosamine reductase (EC 1.1.1.158) (UDP-N-
acetylmuramate dehydrogenase).
GN MURB OR PA2377.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10384043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Cell wall formation (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC -!- COFACTOR: FAD (By similarity).
CC -!- PATHWAY: Peptidoglycan biosynthesis.

protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.

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EMBL; D10988; BAA01761.1; --
PIR; A40250; GNWJ38.
HSSP; P27958; 1HEI.
MEROPS; S29.001; --
MEROPS; U39.001; --
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV env.
InterPro; IPR002531; HCV NS1.
InterPro; IPR002518; HCV NS2.
InterPro; IPR000745; HCV NS4a.
InterPro; IPR001490; HCV NS4b.
InterPro; IPR002868; HCV NS5a.
InterPro; IPR002166; HCV RdRp.
InterPro; IPR004109; Peptidase C29.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSVir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RdRp; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDc1; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane; Nonstructural
INIT_MET 1 1
CHAIN 1 115
CHAIN 116 191
CHAIN 192 383
CHAIN 384 733
CHAIN 734 1010
CHAIN 1011 1619
CHAIN 1620 1866
CHAIN 1867 2017
CHAIN 2018 3033
CHAIN 3034 369
TRANSMEM 347 369
ACT_SITE 1087 1087
ACT_SITE 1111 1111
ACT_SITE 1169 1169
NP_BIND 1234 1241
SITE 1320 1323
SITE 1323 1323
CARBOHYD 196 196
CARBOHYD 209 209
CARBOHYD 233 233
CARBOHYD 299 299
CARBOHYD 305 305
CARBOHYD 417 417
CARBOHYD 423 423
CARBOHYD 430 430
CARBOHYD 448 448
CARBOHYD 477 477

FT CARBOHYD 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1091 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2038 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 3033 AA; 330177 MW; 1A173E7E3381FD1A CRC64;

Query Match 9.5%; Score 80.5; DB 1; Length 3033;
Best Local Similarity 26.6%; Pred. No. 39;
Matches 41; Conservative 22; Mismatches 64; Indels 27; Gaps 7;

QY 5 LCIDSVLERYLLEAKENITTCGAE---HCSLNENITV-PDTKVAFYAWKRM----- 54
DB 1659 IMTSSWVLGGVLAAYVCLATGCSIIIGRLHNDRVVAVDPKELLYEAFDEMEECASK 1718
QY 55 -----EVGQAAVEVWOG--LALLSEAVLRGQALLVNSQWPELQ-----LHYDKAVSGIARS 104
DB 1719 AALIERGQMAEMLKSKIQLLQQATROAQDIQPAIQSSWPKLSQFWAKHMMNFISGIQY 1778
QY 105 LITLLBALG---AQKEALSPDPAASAAPLRTIT 134
DB 1779 LAGLSTLPGNPAVSMMAFS-----AALTSPFLPTST 1809

Search completed: May 25, 2004, 11:22:05
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M protein - protein search, using sw model

Run on: May 25, 2004, 11:19:03 ; Search time 39 Seconds
(without alignments)
1334.885 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APRRLICDSRVLYLLEAK.....SNFLRGKLYTGCACTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mmc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_todent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	723	85.5	192	Q867B1	Q867b1 equus cabal
2	680.5	80.4	195	Q9GKA2	Q9gka2 oryctolagus
3	680.5	80.4	195	Q9GKA3	Q9gka3 oryctolagus
4	678	80.1	194	Q9MYM8	Q9mym8 sus scrofa
5	663	78.4	133	Q8H288	Q8h288 gorilla gor
6	658	77.8	133	Q8H289	Q8h289 pan troglod
7	627	74.1	131	Q8H287	Q8h287 pongo pygma
8	607	71.7	133	Q8H286	Q8h286 macaca sp.
9	554	65.5	133	Q8H285	Q8h285 saquinus oe
10	188	22.2	50	Q9QV40	Q9qv40 rattus sp.
11	88	10.4	323	Q8ZDC8	Q8zdc8 yersinia pe
12	87.5	10.3	346	Q8ZK24	Q8zk24 salmonella
13	87.5	10.3	346	Q8ZK25	Q8zk25 salmonella
14	85	10.0	3722	P94873	P94873 lysobacter
15	83	9.8	296	Q8ZAV4	Q8zav4 yersinia pe
16	82.5	9.8	154	Q87AY9	Q87ay9 xylella fas

ALIGNMENTS

RESULT 1

Q867B1 ID Q867B1 PRELIMINARY; PRT; 192 AA.
AC Q867B1;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Erythropoietin.
GN EPO.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Sato F.;
RT "Equus caballus mRNA for erythropoietin, complete cds."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB100030; BAC55239.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;

Query Match 85.5%; Score 723; DB 6; Length 192;
Best Local Similarity 84.8%; Pred. No. 8.4e-63;
Matches 140; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYLLEAKAEANITTCAGHCSLNENITVPDTKNFYAKMEVQQA 60

Db 27 APRRLICDSRVLYLLEAKAEANITTCAGHCSLNENITVPDTKNFYAKMEVQQA 86

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSLRLTLRLALGAQKEAIS 120

Q7ZUK7 brachydanio
Q9DHD6 hepatitis c
Q9FK91 arabidopsis
Q8J1J9 saccharomyc
Q8DHE3 synchococc
Q7718 hepatitis c
Q77H9 hepatitis c
Q88J10 pseudomonas
Q8UJ6 rhodospirillum rubrum
Q86808 streptomyces
Q91ZAL hepatitis c
Q7710 hepatitis c
Q43380 avena sativ
Q81713 caenorhabditis elegans
Q81715 caenorhabditis elegans
Q8431 mus musculus
Q8299 salmonella
Q80213 mus musculus
Q9529 hepatitis c
Q7772 hepatitis c
Q7717 hepatitis c
Q7716 hepatitis c
Q77H6 hepatitis c
Q77H5 hepatitis c
Q77H4 hepatitis c
Q77H3 hepatitis c
Q86751 streptomyces
Q8ZK3 pyrobaculum
Q8UBQ9 agrobacterium

Db 87 VEVWQGLALLSEALIQGALLANSSQSPETLRLHVDKAVSLRSLTLLRALGAQKEAIS 146
QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 147 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 191
RESULT 2
Q9GKA2 PRELIMINARY; PRT; 195 AA.
AC Q9GKA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO Gene and cDNA: Expression of Rabbit EPO after
RT Intramuscular Injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAC36961.1; -.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; P300272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21025 MW; 1FIDC7F403A303EC CRC64;
Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60
Db 29 APARLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 88
QY 61 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 148
QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 194
RESULT 3
Q9GKA3 PRELIMINARY; PRT; 195 AA.
AC Q9GKA3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO Gene and cDNA: Expression of Rabbit EPO after
RT Intramuscular Injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAC36961.1; -.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; P300272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21025 MW; 1FIDC7F403A303EC CRC64;
Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60
Db 29 APARLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 88
QY 61 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 148
QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 194
RESULT 4
Q9MYM8 PRELIMINARY; PRT; 194 AA.
AC Q9MYM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN LANDRACE; TISSUE=Kidney;
RA David B., Harbitz I.;
RT "The porcine erythropoietin gene: cDNA and genomic sequences and
RT expression analyses";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249745; CAB96416.1; -.
DR EMBL; AJ249746; CAB96417.1; -.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; P300272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 194 AA; 21303 MW; 77881A6F6F20EA1C CRC64;
Query Match 80.1%; Score 678; DB 6; Length 194;
Best Local Similarity 82.0%; Pred. No. 2.2e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60

RT Intramuscular Injection of pDNA."; Biochem. Biophys. Res. Commun. 284:823-827(2001).
RL EMBL; AF290943; AAC36961.1; -.
DR PIR; JC7699; JC7699.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; P300272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60
Db 29 APARLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 88
QY 61 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEALVIRGQALLVNSQFWEPLQHVVDKAVSLRSLTLLRALGAQKEAIS 148
QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 194
RESULT 4
Q9MYM8 PRELIMINARY; PRT; 194 AA.
AC Q9MYM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN LANDRACE; TISSUE=Kidney;
RA David B., Harbitz I.;
RT "The porcine erythropoietin gene: cDNA and genomic sequences and
RT expression analyses";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249745; CAB96416.1; -.
DR EMBL; AJ249746; CAB96417.1; -.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; P300272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 194 AA; 21303 MW; 77881A6F6F20EA1C CRC64;
Query Match 80.1%; Score 678; DB 6; Length 194;
Best Local Similarity 82.0%; Pred. No. 2.2e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60

```
b 27 APRRLCDISVLEYLEAKEGENATMGCAECSSENITVPTDKVNFYAKRMEVQQA 86
y 61 VEVNQGLALSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAIS 120
b 87 VEVNQGLALSEAILQOALLANSQPSALQLHVDKAVSGLSRLTLLRALGAQKAIP 146
y 121 PPDA--ASAPIETITADTFKRLFRYSNPLRCKLKYTGACRTGD 165
b 147 LPDASPSSATPLRTFAVDTLCKLFRYSNPLRCKLKYTGACRRRD 193

RESULT 5
QH288 PRELIMINARY; PRT; 133 AA.
AC QH288;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092016; AA076633.1; -.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 14696 MW; E2D0130942693140 CRC64;

Query Match 78.4%; Score 663; DB 6; Length 133;
Best Local Similarity 99.2%; Pred. No. 4e-57;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 60

y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 120

y 129 PLRTITADTFKRL 141
b 121 PLRTITADTFKRL 133

RESULT 6
QH289 PRELIMINARY; PRT; 133 AA.
AC QH289;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 74.1%; Score 627; DB 6; Length 131;
Best Local Similarity 95.5%; Pred. No. 1.3e-53;
Matches 126; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 58

y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 120
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RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092015; AA076632.1; -.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 14523 MW; ECD5609596390EB CRC64;

Query Match 77.8%; Score 658; DB 6; Length 133;
Best Local Similarity 99.2%; Pred. No. 1.2e-56;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 60

y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 120

y 129 PLRTITADTFKRL 141
b 121 PLRTITADTFKRL 133

RESULT 7
QH287 PRELIMINARY; PRT; 131 AA.
AC QH287;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092017; AA076634.1; -.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 131
SQ SEQUENCE 131 AA; 14403 MW; 143F5E4931EA03FA CRC64;

Query Match 74.1%; Score 627; DB 6; Length 131;
Best Local Similarity 95.5%; Pred. No. 1.3e-53;
Matches 126; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTDKVNFYAKRMEVQQA 58

y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAISPPDAASAA 120
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DB 59 LLSEAVLRGQALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEASPPDAALAA 118
 QY 129 PLRTITADTFK 140
 DB 119 PLRTITADTFK 130
 RESULT 8
 Q8H286 PRELIMINARY; PRT; 133 AA.
 AC Q8H286;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Erythropoietin (Fragment).
 OS Macaca sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9549;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'huigin C., Tichy H., Klein J.;
 RT "Molecular evolution in higher primates; gene specific and organism
 specific characteristics."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY092018; AAM76635.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PRO0272; ERYTHROPTN.
 FT NON_TER 1
 FT NON_TER 133
 SQ SEQUENCE 133 AA; 14506 MW; 55CB11A2DC8354A0 CRC64;
 Query Match 71.7%; Score 607; DB 6; Length 133;
 Best Local Similarity 90.2%; Pred. No. 1.2e-51;
 Matches 120; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 9 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAQVFWQGLA 68
 DB 1 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAQVFWQGLA 60
 QY 69 LLSEAVLRGQALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAISPPDAASAA 128
 DB 61 LLSEAVLRGQAVLANSOPFFPLQLHMDKASGLRSITLLRALGAQKEAISPPDAASAA 120
 QY 129 PLRTITADTFK 141
 DB 121 PLRTITADTFK 133
 RESULT 9
 Q8H285 PRELIMINARY; PRT; 133 AA.
 AC Q8H285;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Erythropoietin (Fragment).
 OS Saguinus oedipus (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=9490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'huigin C., Tichy H., Klein J.;
 RT "Molecular evolution in higher primates; gene specific and organism
 specific characteristics."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY092019; AAM76636.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PRO0272; ERYTHROPTN.
 FT NON_TER 1
 FT NON_TER 133
 SQ SEQUENCE 133 AA; 14375 MW; C923E859BB608FEC CRC64;
 Query Match 65.5%; Score 554; DB 6; Length 133;
 Best Local Similarity 84.3%; Pred. No. 1.9e-46;
 Matches 111; Conservative 8; Mismatches 11; Indels 2; Gaps 2;
 QY 9 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAQVFWQGLA 68
 DB 1 SGVLYRYVLEGEAEENVTCGACSSCNENITVPTDKNFYAKRMVEVQQAQVFWQGLT 60
 QY 69 LLSEAVLRGQALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAISPPDAASAA 127
 DB 61 LLSEAVLRGQALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAISPPDAASAA 119
 QY 128 APLRTITADTFK 141
 DB 120 VPLQITADTFK 133
 RESULT 10
 Q9QV40 PRELIMINARY; PRT; 50 AA.
 AC Q9QV40;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Erythropoietin (fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94115047; PubMed=7764337;
 RA Okano M., Suga H., Masuda S., Nagao M., Narita H., Ikura K.,
 RA Sasaki R.;
 RL Biosci. Biotechnol. Biochem. 57:1882-1885 (1993).
 DR HSP; P01588; 1EER.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PRO0272; ERYTHROPTN.
 SQ SEQUENCE 50 AA; 5587 MW; 70B44A8BFE016034 CRC64;
 Query Match 22.2%; Score 188; DB 11; Length 50;
 Best Local Similarity 78.0%; Pred. No. 4.2e-11;
 Matches 39; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 APRPLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFY 50
 DB 1 APRPLIXDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFY 50
 RESULT 11
 Q8ZDC8 PRELIMINARY; PRT; 323 AA.
 ID Q8ZDC8;
 AC Q8ZDC8;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1).
NRDF OR YP02648 OR Y1222.
S Yersinia pestis.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Yersiniaceae.
X NCBI_TaxID=632;
[1]
P SEQUENCE FROM N.A.
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586360;
A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prenice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
A Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
T "Genome sequence of Yersinia pestis, the causative agent of plague.";
L Nature 413:523-527(2001).
[2]
N SEQUENCE FROM N.A.
P STRAIN=KIMS / Biovar Mediaevalis;
C MEDLINE=22137863; PubMed=12142430;
X Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
A Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
A Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Blattner F.R.,
A Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Barrell B.G.,
A Perry R.D.;
T "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
R EMBL: AJ414153; CAC92889.1; -;
R EMBL: AE013726; AM84798.1; -;
R PIR: AB0323; AB0323.
R GO: GO:0016491; F:oxidoreductase activity; IEA.
R GO: GO:0004748; F:ribonucleoside-diphosphate reductase activity; IEA.
R GO: GO:0009186; P:deoxyribonucleoside diphosphate metabolism; IEA.
R InterPro: IPR000358; RibonucL reductase.
R Pfam: PF00268; ribonuc red sm; 1.
R PROSITE: PS00368; RIBORED_SMALL; 1.
R Oxidoreductase; Complete Proteome
W SEQUENCE 323 AA; 36823 MW; 87C21F7BBB9B7FD2 CRG64;
Q SEQUENCE 323 AA; 36823 MW; 87C21F7BBB9B7FD2 CRG64;
Query Match 10.4%; Score 88; DB 16; Length 323;
Best Local Similarity 25.2%; Pred. No. 2.8;
Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;
Y 38 NITVPDTKYNFAWKMEVQQAWEVWQGLALLSEAVLQGLVNSSQPWEFLQLHVD- 96
b 2 NVVKPITRISAINWNKIE-DKOLEVWN--RLTSNFWLPKVPVLSNDIPSWATLTPHEQQ 58
Y 97 ---KAVSLRSLTLRLALGQA---KEAIFPPDAAGAPLRTITADTFKLFVYSNFLR 150
b 59 LTRVFTGLTLDITQNTLGPALIKDAITPHEAIFSNISFMEAVHARSYSSIFSTL-- 116
Y 151 GKILKLYTGEACRTGD 165
b 117 -----CLTSD 121
RESULT 12
Q8ZKZ4
ID Q8ZKZ4 PRELIMINARY; PRT; 346 AA.
AC Q8ZKZ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Periplasmic sensor in multi-component regulatory system with Tors
DE (Sensory kinase) and Tors (Regulator), regulates tor operon.
EN TORS OR STM3825.
CS Salmonella typhimurium.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Salmonella.
CX NCBI_TaxID=602;

SEQUENCE FROM N.A.
RN NRDF OR YP02648 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Courtney L., Parkhill S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
L72.";
RL Nature 413:852-856(2001).
DR EMBL: AE008878; AAL22684.1; -;
DR InterPro: IPR001761; PeriplaBP/LacI.
DR Pfam: PF00332; Peripla_BP_like; 1.
KW Complete proteome.
SQ SEQUENCE 346 AA; 38440 MW; E37CAB58E49FD716 CRC64;
Query Match 10.3%; Score 87.5; DB 16; Length 346;
Best Local Similarity 26.7%; Pred. No. 3.4;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;
QY 10 RVLRYLLEAKAEANITTG--CAEHCSLNE--NITVPDTKYNFAWKMEVQQAWEVWQ 65
b 217 RNLQEMLERHPDANVAVGSAIAEAMGEGRNLTPLTIVSYFL-----THQVYR 267
QY 66 GLALLSEAVLQGLVNSSQ-PWEFLQLHVDKAVSGLSLTLRLALGQA--KEAIFPP 122
b 268 GLK-----RGHILMALSDQAWQ-----GELAITQSIKVLQGPVFNISPP 309
QY 123 -----DAASAAPLRTITADTFKLFVYSNFLRGLKLYTGEA 160
b 310 VLTLTHNADSRVRSLSPPGFRPVY-----LYQYTSEA 344
RESULT 13
Q8Z2M5
ID Q8Z2M5 PRELIMINARY; PRT; 346 AA.
AC Q8Z2M5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Solute binding receptor protein.
GN STY3952 OR TORT OR T3693.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
J. Bacteriol. 185:2330-2337(2003).
RL EMBL: AL627280; CAD03169.1; -;

Query Match	10.0%	Score 85	DB 2	Length 3722
Best Local Similarity	22.1%	Pred. No. 1.2e+02		
Matches 34	Conservative 18	Mismatches 50	Indels 52	Gaps 5
QY	16	LLKAKAEINITGCAEHCSLNENIIVPTKVFYAKRMVEYQQAQVEV----	WQGLALLS 71	
DB	2138	LLSGATAQLP-----PLPATYADFQWQORQLSDQLDALFDYQW-----	2178	
QY	72	EAVLRQALLVNSQPWEPLQHVDKAVGSLRSTTLRLALGAQ-----	KEATSPDPAAS 126	
DB	2179	-----RSLAQWQPLFLD-----HARPAQFDYLGREIVFDVDATT 2214		
QY	127	AAPLRTITADTFKPLFRVYSNLRGKMLKLYTGEA 160		
DB	2215	CDQIRVLACTRTSPFVLLAAYITLKAYSQS 2248		
RESULT 15				
Q8ZAY4	ID	Q8ZAY4	PRELIMINARY;	PRT; 296 AA.
AC	Q8ZAY4			
DT	01-MAR-2002	(TEMBLrel. 20, Created)		
DT	01-MAR-2002	(TEMBLrel. 20, Last sequence update)		
DT	01-JUN-2003	(TEMBLrel. 24, Last annotation update)		
DE	Putative 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	(Putative oxidoreductase).		
DE	Yersinia pestis.			
GN	YPO3648 OR Y0219.			
OS	Yersinia pestis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Yersinia.			
OX	NCBI_TaxID=632;			
RN	[1]	SEQUENCE FROM N.A.		
RC	STRAIN=CO-92 / Biovar Orientalis;			
RC	MEDLINE=21470413; PubMed=11586360;			
RX	Parkhill J.B., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,			
RA	Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,			
RA	Leather S., Moulé S., Oyston P.C.F., Quail M., Rutherford K.,			
RA	Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;			
RA	"Genome sequence of Yersinia pestis, the causative agent of plague.";			
RT	Nature 413:523-527(2001).			
RN	[2]	SEQUENCE FROM N.A.		
RP	STRAIN=KIM5 / Biovar Mediaevalis;			
RC	MEDLINE=22137863; PubMed=12142430;			
RX	Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,			
RA	Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,			
RA	Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,			
RA	Straley S.C., McDonough K.A., Milles M.L., Matson J.S., Blattner F.R.,			
RA	Perry R.D.;			
RA	"Genome sequence of Yersinia pestis KIM.";			
RT	J. Bacteriol 184:4501-4511(2002).			
RL	EMBL; AJ414158; CAC93117.1; -			
DR	EMBL; AE013622; AAM8381.1; -			
DR	PIR; A10443; A10443.			
DR	GO; GO:0008679; F:2-hydroxy-3-oxopropionate reductase activity; IEA.			
DR	GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.			
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR	GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.			
DR	GO; GO:0006038; P:phosphate shunt; IEA.			
DR	GO; GO:0006573; P:valine metabolism; IEA.			
DR	InterPro; IPR002204; 3hydroxisobut_dh.			
DR	InterPro; IPR006115; 6PGD_NAD.			
DR	Pfam; PF03446; NAD binding 2; 1.			
DR	PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.			
KW	Hypothetical protein; Oxidoreductase; Complete proteome.			
SEQ	SEQUENCE 296 AA; 32140 MW; C883AFCC868429D CRC64;			
Query Match	9.8%	Score 83	DB 16	Length 296;

Best Local Similarity 24.2%; Pred. No. 7.8;
Matches 48; Conservative 34; Mismatches 62; Indels 54; Gaps 10;

y	6	ICDSRVLERVLLLEAK-EAENITTCGAHCHSLNENIT-VPDTKVNFYAWKMEVGOQAVEV	63
b	32	LCDAITKVOILTAEINABSLVDNA--ASLDALITMFPNSE-----AVEQVLLGSDGISG	85
y	64	WQGLALLSEAVLRGOALLVNSQF-----WE-----PLQLHVDKAVSG----	101
b	86	W--VAQLSQAAV--VIDMSSDPERSRRLAILLAVWELDYLDAPVSGGVKKAQNGTLSI	140
y	102	-----LRSLTLLRALGAQKEAISPDAASAAP-----LRTITADTFRKLP	142
b	141	LIGGEDRVLXSCYTALAAMGEQILFVGPAGSGHAAKALANNVVSATGLLATIEALHVAQRF	200
y	143	RVYSNFLRGKLYTGEA	160
b	201	GIEPEVMTVINTSTGRS	218

earch completed: May 25, 2004, 11:23:00
ob time : 43 secs

M protein - protein search, using sw model

run on: May 25, 2004, 11:19:33 ; Search time 20 seconds
(without alignments)
793.580 Million cell updates/sec

title: US-09-830-964-1

effect score: 846

sequence: 1 APPRLICDSRVLEYLEAK.....SNFLRGKLYTGACRTGD 165

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	193	1 ZUHU	erythropoietin pre
2	764.5	90.4	192	1 JQ0173	erythropoietin pre
3	759.5	89.8	192	1 184613	erythropoietin pre
4	713	84.3	188	1 146083	erythropoietin pre
5	701	82.9	192	1 S28148	erythropoietin pre
6	685.5	81.0	194	1 146401	erythropoietin pre
7	681	80.5	192	1 A24902	erythropoietin pre
8	680.5	80.4	193	2 J76999	erythropoietin - r
9	678	80.1	190	2 146578	erythropoietin - p
10	638	75.4	175	2 146199	erythropoietin - d
11	90	10.6	353	2 G02729	thrombopoietin - h
12	89	10.5	353	2 180105	thrombopoietin pre
13	88	10.4	323	2 AB0323	ribonucleoside-dip
14	87.5	10.3	345	2 AE0359	Solute binding rec
15	86	10.2	286	2 A55330	megakaryocyte grow
16	83	9.8	296	2 A10443	probable 2-hydroxy
17	83	9.8	339	2 AB3274	UDP-N-acetylpyruvo
18	80.5	9.5	3033	1 GNWJ08	genome polyprotein
19	79.5	9.4	1829	2 T35681	probable sensory h
20	79	9.3	480	2 S56639	ribosomal protein
21	78.5	9.3	813	2 AF0526	ATP-dependent heli
22	78.5	9.3	897	2 A54896	EGF receptor subst
23	78	9.2	348	2 T35450	ABC transporter Ar
24	78	9.2	455	2 AG2919	conserved hypothet
25	78	9.2	455	2 H97693	methylamine utiliz
26	78	9.2	747	1 S36741	probable copper-tr
27	77.5	9.2	242	2 AD1928	hypothetical prote
28	77	9.1	451	2 S75569	hypothetical prote
29	76.5	9.0	154	2 H82810	bacterioferritin X

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C/Species: Homo sapiens (man)

C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000

C/Accession: A01855; A24744; A25384; A22210; S56178

R/Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; Seel
Nature 313, 806-810, 1985

A/Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A/Reference number: A01855; MUID:85137899; PMID:3838366

A/Accession: A01855

A/Molecule type: mRNA; DNA

A/Residues: 1-193 <JAC>

A/Cross-references: GB:X02157; GB:X02158

R/Lin, P.K.; Sugars, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; I
Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A/Title: Cloning and expression of the human erythropoietin gene.

A/Reference number: A24744; MUID:86067948; PMID:3865178

A/Accession: A24744

A/Molecule type: DNA

A/Residues: 1-193 <LIN>

A/Cross-references: GB:M11319; NID:g182197; PIDN:AAA52400.1; PID:g182198

R/Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A/Title: Structural characterization of human erythropoietin.

A/Reference number: A25384; MUID:86140080; PMID:3949763

A/Accession: A25384

A/Molecule type: protein

A/Residues: 28-86, 'Q', 87-193 <LAI>

A/Experimental source: urine

A/Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R/Yanagawa, S.; Hirade, K.; Ohnaka, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A/Title: Isolation of human erythropoietin with monoclonal antibodies.

A/Reference number: A22210; MUID:84135751; PMID:6698989

A/Accession: A22210

A/Molecule type: protein

A/Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R/Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A/Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A/Reference number: S56178; MUID:95284365; PMID:7766897

A/Accession: S56178

A/Molecule type: protein

A/Residues: 28-33, 'X', 35-37 <WTS>

C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C/Genetics:

A/Gene: GDB:EPO

A/Cross-references: GDB:119110; OMIM:133170

A/Map position: 7q21.3-7q22.1

A/Introns: 5/1; 53/3; 82/3; 142/3

C/Function:

```
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status experimental
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-74; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 147

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165
Db 148 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 192

RESULT 2
JQ0173
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-SEP-1990 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.;
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:G342093; PIDN:AAA368
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 764.5; DB 1; Length 192;
Best Local Similarity 91.5%; Pred. No. 1.7e-66; Indels 1; Gaps 1;
Matches 151; Conservative 7; Mismatches 6;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165
Db 147 LPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 191

erythropoietin precursor - rhesus macaque

RESULT 3
I84613
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: GB:L10609; NID:G342095; PIDN:AAA36842.1; PID:G342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.8%; Score 759.5; DB 1; Length 192;
Best Local Similarity 90.3%; Pred. No. 5.1e-66; Indels 1; Gaps 1;
Matches 149; Conservative 9; Mismatches 6;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLSRLTLLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165
Db 147 LPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 191

erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: GB:L10606; NID:G163820; PIDN:AAA30807.1; PID:G163821
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-193,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 713; DB 1; Length 188;
Best Local Similarity 84.2%; Pred. No. 1.6e-61; Indels 0; Gaps 0;
Matches 139; Conservative 9; Mismatches 17;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 23 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 82
```

A:Residues: 1-194 <FX>
 A:Cross-references: EMBL:724581; NID:g9395049; PIDN:CAA80848.1; PID:g9395050
 R;Wen, D.; Bolissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I47077
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
 A:Cross-references: GB:L10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-194/Product: erythropoietin #status predicted <MAT>
 F:34-189,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:154/Binding site: carbohydrate (Ser) (covalent) #status predicted
 Query Match 81.0%; Score 685.5; DB 1; Length 194;
 Best Local Similarity 81.9%; Pred. No. 7,4e-59;
 Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 Qy 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 60
 Db 28 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVQQA 87
 Qy 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVGSLRSLTLTLRALGAQKEAIS 120
 Db 88 LEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVGSLRSLTLTLRALGAQKEAIS 147
 Qy 121 PPDAASAPLRTITADTFKLFVYNSFLRGLKLYTGEACRTGD 165
 Db 148 LPDAPSAAPLRTITADTFKLFVYNSFLRGLKLYTGEACRTGD 193
 RESULT 7
 A24902
 A:Title: Erythropoietin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: A24901
 R:Shoemaker, C.B.; Mitsock, L.D.
 Mol. Cell. Biol. 6, 849-858, 1986
 A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
 A:Reference number: A24502; MUID:87039105; PMID:3773894
 A:Accession: A24902
 A:Molecule type: DNA
 A:Residues: 1-192 <SHO>
 A:Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 as
 R;McDonald, J.D.; Lin, F.K.; Goldwasser, E.
 Mol. Cell. Biol. 6, 842-848, 1986
 A:Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
 A:Reference number: A24901; MUID:87039104; PMID:3022133
 A:Accession: A24901
 A:Molecule type: DNA
 A:Residues: 1-67, 'P', 69-192 <MCD>
 A:Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver
 C:Genetics:
 A:Introns: 5/1; 52/3; 81/3; 141/3
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted
 A:Status: translated from GB/EMBL/DBDJ

```
Query Match      80.5%; Score 681; DB 1; Length 192;
Best Local Similarity 79.4%; Pred. No. 2e-58;
Matches 131; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 60
DB 27 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 120
DB 87 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 146
QY 121 PPDAASAAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 165
DB 147 PPDTPPAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 191

RESULT 8
JC7699
erythropoietin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C:Accession: JC7699
R:Vitala, A.; Wu, D.; Margalith, M.; Hobart, P.
Biochem. Biophys. Res. Commun. 284, 823-827, 2001
A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
A:Reference number: JC7699; MUID:21290682; PMID:11396976
A:Contents: Kidney
A:Accession: JC7699
A:Molecule type: DNA
A:Residues: 1-195 <VIL>
A:Cross-references: GB:AF290943
C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
cytes.
C:Genetics:
A:Gene: epo
C:Superfamily: erythropoietin
C:Keywords: glycoprotein; kidney

Query Match      80.4%; Score 680.5; DB 2; Length 195;
Best Local Similarity 81.3%; Pred. No. 2.3e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 60
DB 29 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 120
DB 89 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 148
QY 121 PPDAASAAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 165
DB 149 PPEAASAAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 194

RESULT 9
I46578
erythropoietin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46578
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46578
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <WEN>
A:Cross-references: GB:I10607; NID:g164445; PIDN:AAA31029.1; PID:g164446
C:Superfamily: erythropoietin

Query Match      80.1%; Score 678; DB 2; Length 190;
Best Local Similarity 82.0%; Pred. No. 3.8e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 82
QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 120
DB 83 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 142
QY 121 PPDAASAAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 165
DB 143 LPDASPSSAPLRTITADTFPRKLFVYSNFRGKGLKLYTGEACRTGD 189

RESULT 10
I46199
erythropoietin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46199
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46199
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <WEN>
A:Cross-references: GB:I13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
C:Superfamily: erythropoietin

Query Match      75.4%; Score 638; DB 2; Length 175;
Best Local Similarity 81.0%; Pred. No. 2.6e-54;
Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 82
QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRALGAQKEAIS 120
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QY 121 PPDAASAAPLRTITADTFPRKLFVYSNFRGKGL 153
DB 143 LPEASAPLRTITADTFPRKLFVYSNFRGKGL 175

RESULT 11
G02729
thrombopoietin - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02729
R:Im, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01637
A:Accession: G02729
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <IMX>
A:Cross-references: EMBL:U59493; NID:g1401245; PIDN:AA03392.1; PID:g1401246
C:Genetics:
A:Gene: HPO

Query Match      10.6%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.61;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCHSLNENITVPDTKYNFYAKRMEVQQA 60
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Query Match 10.5%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.76; Mismatches 20; Indels 20; Gaps 5;
Matches 41; Conservative 20; Mismatches 20; Indels 20; Gaps 5;
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Qy 61 VEVWQGLALLSEAVL--RQALLVNSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEA 118
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQLSQVRLLLGALQSL-----LGTQ--- 132
Qy 119 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGK 154
Db 133 -LPPOG-----RTTAHKDPNAIFLSFOHLLRGKVR 161
RESULT 12
80105
hombopoietin precursor - human
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;Species: Homo sapiens (man)
;Date: 24-May-1996 #sequence revision 24-May-1996 #text change 20-Jun-2000
;Accession: I59281; I80105; S45331; S48740; I38672; I52610
;Poster: D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kujper, J.L.; Holly, R.D.; W
roc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
;Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosoma
;Reference number: I59281; MUID:95108091; PMID:7809166
;Accession: I59281
;Status: translated from GB/EMBL/DDBJ
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;Status: preliminary
;Molecule type: mRNA
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;Cross-references: GB:I33410; NID:G506826; PIDN:AAAS9857.1; PID:G506827
;Schma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
EBS Lett. 353, 57-61, 1994
;Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
;Reference number: S48740; MUID:95010765; PMID:7926023
;Accession: S48740
;Status: preliminary
;Molecule type: DNA
;Residues: 1-353 <SOH>
;Cross-references: GB:D32046; NID:G577319; PIDN:BAA06807.1; PID:G577320
;Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
elli 77, 1117-1124, 1994
;Title: Identification and cloning of a megakaryocyte growth and development factor tha
;Reference number: A54463; MUID:94291201; PMID:8020099
;Accession: I38672
;Status: preliminary
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;Residues: 1-112, 'E', 114-353 <RE3>
;Cross-references: EMBL:U11025; NID:G511223; PIDN:AAAS0553.1; PID:G558078
;Gurney, A.L.; Huang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
lood 85, 981-988, 1995
;Title: Genomic structure, chromosomal localization, and conserved alternative splice f
;Reference number: I52610; MUID:95152076; PMID:7849319
;Accession: I52610
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;Molecule type: DNA
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;Gene: GDB:THPO; MGDF
;Cross-references: GDB:374007; OMIM:600044

A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein
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Best Local Similarity 26.3%; Pred. No. 0.76; Mismatches 20; Indels 20; Gaps 5;
Matches 41; Conservative 20; Mismatches 20; Indels 20; Gaps 5;
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Qy 61 VEVWQGLALLSEAVL--RQALLVNSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEA 118
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92889.1; PID:G15980631; GSPDB:GN00175
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C;Superfamily: ribonucleoside-diphosphate reductase beta
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Qy 97 ---KAVSGLSRLTTLRALGAQ---KEATSPDDAASAPLRTITADTFKRLFRVYSNFLR 150
Db 59 LTRVFTGLTLDITQTLGAPALIKDALTPEEAIFSNISFMBAVHARSYSIFSTL-- 116
Qy 151 GKUKLYTGACRTGD 165
Db 117 -----CLTSD 121
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Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0359
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovi

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Job time : 24 secs

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M protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

searched: 1149313 seqs, 278921704 residues

total number of hits satisfying chosen parameters: 1149313

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ost-processing: Minimum Match 0%
Maximum Match 100%
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 - 2: /cgn2_6/prodata/2/pubpaa/BCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
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 - 17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	9	US-09-853-731-1
2	846	100.0	165	10	US-09-945-517-1
3	846	100.0	165	12	US-10-411-037-73
4	846	100.0	165	13	US-10-411-028-73
5	846	100.0	165	13	US-10-014-363-1
6	846	100.0	165	14	US-10-241-356-1
7	846	100.0	165	14	US-10-293-551-1
8	846	100.0	165	16	US-10-410-962-73
9	846	100.0	165	16	US-10-411-049-73
10	846	100.0	166	9	US-09-853-731-2
11	846	100.0	166	12	US-10-467-115-1
12	846	100.0	166	13	US-10-014-363-2
13	846	100.0	166	14	US-10-241-356-2
14	846	100.0	166	14	US-10-293-551-2
15	846	100.0	165	14	US-10-400-377-2

16	846	100.0	166	14	US-10-400-708-2	Sequence 2, Appli
17	846	100.0	166	14	US-10-298-148-2	Sequence 2, Appli
18	846	100.0	166	15	US-10-360-101-227	Sequence 227, App
19	846	100.0	169	13	US-10-014-363-4	Sequence 4, Appli
20	846	100.0	174	13	US-10-014-363-3	Sequence 3, Appli
21	846	100.0	174	13	US-10-014-363-5	Sequence 5, Appli
22	846	100.0	193	10	US-09-813-775C-4	Sequence 4, Appli
23	846	100.0	193	14	US-10-113-824-2	Sequence 2, Appli
24	846	100.0	209	14	US-10-230-454-4	Sequence 4, Appli
25	846	100.0	220	14	US-10-196-183-2	Sequence 2, Appli
26	846	100.0	370	14	US-10-230-454-3	Sequence 3, Appli
27	846	100.0	428	12	US-10-622-108-10	Sequence 10, Appli
28	846	100.0	428	15	US-10-435-608-10	Sequence 10, Appli
29	846	100.0	435	10	US-09-932-812-22	Sequence 22, Appli
30	846	100.0	436	10	US-09-932-812-18	Sequence 18, Appli
31	846	100.0	437	10	US-09-932-812-20	Sequence 20, Appli
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35	843	99.6	425	12	US-10-622-108-8	Sequence 8, Appli
36	843	99.6	425	15	US-10-435-608-8	Sequence 8, Appli
37	838	99.1	166	15	US-10-455-697-1	Sequence 1, Appli
38	838	99.1	166	16	US-10-291-847-214	Sequence 214, App
39	838	99.1	166	16	US-10-460-550-3	Sequence 3, Appli
40	838	99.1	193	10	US-09-813-775C-2	Sequence 2, Appli
41	838	99.1	193	12	US-10-411-037-16	Sequence 16, Appli
42	838	99.1	193	12	US-10-411-026-16	Sequence 16, Appli
43	838	99.1	193	12	US-10-609-346-16	Sequence 16, Appli
44	838	99.1	193	15	US-10-351-196-2	Sequence 2, Appli
45	838	99.1	193	15	US-10-463-980-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

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Query Match	100.0%	Score 846;	DB 9;	Length 165;
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US-10-411-037-73

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RESULT 4
 US-10-411-026-73
 ; Sequence 73, Application US/10411026
 ; Publication No. US20040063911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
 ; TITLE OF INVENTION: METHODS
 ; FILE REFERENCE: 040853-01-5053
 ; CURRENT APPLICATION NUMBER: US/10/411,026
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-411-026-73

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RESULT 3
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 ; Sequence 73, Application US/10411037
 ; Publication No. US20040043446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Garyn
 ; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
 ; TITLE OF INVENTION: GALACTOSIDASE A
 ; FILE REFERENCE: 040853-01-5082
 ; CURRENT APPLICATION NUMBER: US/10/411,037
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
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 ; PRIOR FILING DATE: 2002-07-17
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 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-945-517-1

JS-09-945-517-1
 ; Sequence 1, Application US/09945517
 ; Publication No. US20030104996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Tiansheng
 ; APPLICANT: Chang, Byeong
 ; APPLICANT: Sloey, Christopher
 ; TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
 ; FILE REFERENCE: A-803
 ; CURRENT APPLICATION NUMBER: US/09/945,517
 ; CURRENT FILING DATE: 2001-08-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.0
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 ; LENGTH: 165
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 ; ORGANISM: Homo sapiens
 ; US-09-945-517-1

RESULT 5
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 Publication No. US20020115833A1
 GENERAL INFORMATION:
 APPLICANT: Burg, Josef
 APPLICANT: Engel, Alfred
 APPLICANT: Franze, Reinhard
 APPLICANT: Hilger, Bernd
 APPLICANT: Schurig, Hartmut Ernst
 APPLICANT: Tischer, Wilhelm
 APPLICANT: Wozny, Manfred
 TITLE OF INVENTION: Erythropoietin Conjugates
 FILE REFERENCE: Case 20805
 CURRENT APPLICATION NUMBER: US/10/014,363
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 Query Match 100.0%; Score 846; DB 13; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 6
 S-10-241-356-1
 Sequence 1, Application US/10241356
 Publication No. US2003007753A1
 GENERAL INFORMATION:
 APPLICANT: TISCHER, WILHELM
 TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
 FILE REFERENCE: 20971
 CURRENT APPLICATION NUMBER: US/10/241,356
 CURRENT FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: EP 01122555.4
 PRIOR FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-10-241-356-1
 Query Match 100.0%; Score 846; DB 14; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 7
 US-10-293-551-1
 Sequence 1, Application US/10293551
 Publication No. US20030120045A1
 GENERAL INFORMATION:
 APPLICANT: Bailon, Pascal
 TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 FILE REFERENCE: 1097 nonprovisional
 CURRENT APPLICATION NUMBER: US/10/293,551
 CURRENT FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: US/09/604,938
 PRIOR FILING DATE: 2000-08-27
 PRIOR APPLICATION NUMBER: 60/166,151
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/151,548
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: 60/150,225
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: 60/142,254
 PRIOR FILING DATE: 1999-07-02
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-293-551-1
 Query Match 100.0%; Score 846; DB 14; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 8
 US-10-410-962-73
 Sequence 73, Application US/10410962
 Publication No. US2004007836A1
 GENERAL INFORMATION:
 APPLICANT: Neose Technologies, Inc.
 APPLICANT: DePrees, Shawn
 APPLICANT: Zopf, David
 APPLICANT: Bayer, Robert
 APPLICANT: Hakes, David
 APPLICANT: Chen, Xi
 APPLICANT: Bowe, Caryn
 TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
 TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
 FILE REFERENCE: 040853-01-5054
 CURRENT APPLICATION NUMBER: US/10/410,962
 CURRENT FILING DATE: 2003-04-09
 PRIOR APPLICATION NUMBER: US 60/328,523
 PRIOR FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 60/344,692
 PRIOR FILING DATE: 2001-10-19
 PRIOR APPLICATION NUMBER: US 60/387,292

RESULT 5
 S-10-014-363-1
 Sequence 1, Application US/10014363
 Publication No. US20020115833A1
 GENERAL INFORMATION:
 APPLICANT: Burg, Josef
 APPLICANT: Engel, Alfred
 APPLICANT: Franze, Reinhard
 APPLICANT: Hilger, Bernd
 APPLICANT: Schurig, Hartmut Ernst
 APPLICANT: Tischer, Wilhelm
 APPLICANT: Wozny, Manfred
 TITLE OF INVENTION: Erythropoietin Conjugates
 FILE REFERENCE: Case 20805
 CURRENT APPLICATION NUMBER: US/10/014,363
 CURRENT FILING DATE: 2001-12-11
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-10-014-363-1
 Query Match 100.0%; Score 846; DB 13; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 6
 S-10-241-356-1
 Sequence 1, Application US/10241356
 Publication No. US2003007753A1
 GENERAL INFORMATION:
 APPLICANT: TISCHER, WILHELM
 TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
 FILE REFERENCE: 20971
 CURRENT APPLICATION NUMBER: US/10/241,356
 CURRENT FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: EP 01122555.4
 PRIOR FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-10-241-356-1
 Query Match 100.0%; Score 846; DB 14; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 7
 US-10-293-551-1
 Sequence 1, Application US/10293551
 Publication No. US20030120045A1
 GENERAL INFORMATION:
 APPLICANT: Bailon, Pascal
 TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 FILE REFERENCE: 1097 nonprovisional
 CURRENT APPLICATION NUMBER: US/10/293,551
 CURRENT FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: US/09/604,938
 PRIOR FILING DATE: 2000-08-27
 PRIOR APPLICATION NUMBER: 60/166,151
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/151,548
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: 60/150,225
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: 60/142,254
 PRIOR FILING DATE: 1999-07-02
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-293-551-1
 Query Match 100.0%; Score 846; DB 14; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 b 1 APPRLCDRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Y 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 b 121 PPDAASAPLRITTTADTFKFLFRVYSNFRGLKLYTGACRTGD 165
 RESULT 8
 US-10-410-962-73
 Sequence 73, Application US/10410962
 Publication No. US2004007836A1
 GENERAL INFORMATION:
 APPLICANT: Neose Technologies, Inc.
 APPLICANT: DePrees, Shawn
 APPLICANT: Zopf, David
 APPLICANT: Bayer, Robert
 APPLICANT: Hakes, David
 APPLICANT: Chen, Xi
 APPLICANT: Bowe, Caryn
 TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
 TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
 FILE REFERENCE: 040853-01-5054
 CURRENT APPLICATION NUMBER: US/10/410,962
 CURRENT FILING DATE: 2003-04-09
 PRIOR APPLICATION NUMBER: US 60/328,523
 PRIOR FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 60/344,692
 PRIOR FILING DATE: 2001-10-19
 PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent in version 3.2
SEQ ID NO 73
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-962-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 9
US-10-411-049-73
Sequence 73, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DePree, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent in version 3.2
SEQ ID NO 73
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-049-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 10
US-09-853-731-2
Sequence 2, Application US/09853731
Patent No. US20020037841A1
GENERAL INFORMATION:
APPLICANT: Papadimitriou, Apollon
TITLE OF INVENTION: Erythropoietin Composition
FILE REFERENCE: 20619 US
CURRENT APPLICATION NUMBER: US/09/853,731
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP/00110355.5
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 100.0%; Score 846; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 1 APPRLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 11
US-10-467-115-1
Sequence 1, Application US/10467115
Publication No. US20040063917A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
FILE REFERENCE: MER-114
CURRENT APPLICATION NUMBER: US/10/467,115
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: 01102615.0
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: PCT/EP02/01174

PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
S-10-467-115-1

Query Match 100.0%; Score 846; DB 12; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
b 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 12
S-10-014-363-2
Sequence 2, Application US/10014363
Publication No. US20020115833A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
S-10-014-363-2

Query Match 100.0%; Score 846; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
b 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 13
S-10-241-356-2
Sequence 2, Application US/10241356
Publication No. US2003007753A1
GENERAL INFORMATION:
APPLICANT: TISCHER, WILHELM

TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
FILE REFERENCE: 20971
CURRENT APPLICATION NUMBER: US/10/241,356
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: EP 01122555.4
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 100.0%; Score 846; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 14
US-10-293-551-2
Sequence 2, Application US/10293551
Publication No. US20030120045A1
GENERAL INFORMATION:
APPLICANT: Ballon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/293,551
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/604,938
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 100.0%; Score 846; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 1 APRLLCDRVLRYLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

Db 121 PPDAASAAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

RESULT 15

US-10-400-377-2

; Sequence 2, Application US/10400377

; Publication No. US20030162949A1

; GENERAL INFORMATION:

; APPLICANT: Cox III, George N

; APPLICANT: Bolder Biotechnology, Inc.

; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

; FILE REFERENCE: 4152-1-PUS

; CURRENT APPLICATION NUMBER: US/10/400,377

; CURRENT FILING DATE: 2003-03-26

; PRIOR APPLICATION NUMBER: US/09/462,941

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/052,516

; PRIOR FILING DATE: 1997-07-14

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-400-377-2

Query Match 100.0%; Score 846; DB 14; Length 166;

Best Local Similarity 100.0%; Pred. No. 5.7e-88;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 60

Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSITLLRALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSITLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

Search completed: May 25, 2004, 11:28:52

Job time : 44 secs

M protein - protein search, using sw model

run on: May 25, 2004, 11:20:29 ; Search time 23 Seconds
(without alignments)
370.360 Million cell updates/sec

title: US-09-830-964-1
subject score: 846
sequence: 1 APPRLICDSRVLYRLLEAK.....SNFLRGKLYTGACRTGD 165

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

total number of hits satisfying chosen parameters: 389414

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/aaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/aaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/aaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/aaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/aaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/aaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Match	Query Length	ID	Description
1	846	100.0	165	4	US-09-604-871-1
2	846	100.0	165	4	US-09-604-938-1
3	846	100.0	166	1	US-08-318-193-70
4	846	100.0	166	4	US-09-604-871-2
5	846	100.0	166	4	US-09-604-938-2
6	846	100.0	166	4	US-09-462-941-2
7	846	100.0	166	5	PCT-US94-04361-37
8	846	100.0	193	1	US-07-903-220-1
9	846	100.0	193	2	US-08-883-795A-34
10	846	100.0	193	4	US-09-552-265B-4
11	843	99.6	165	4	US-09-554-451-8
12	843	99.6	412	4	US-09-366-009-34
13	843	99.6	412	4	US-08-809-156B-34
14	838	99.1	193	4	US-09-552-265B-2
15	834	98.6	193	4	US-09-552-265B-4
16	830	98.1	166	5	PCT-US94-04361-45
17	825	97.5	166	4	US-09-552-265B-30
18	825	97.5	193	4	US-09-552-265B-46
19	824	97.4	166	4	US-09-552-265B-22
20	824	97.4	166	4	US-09-552-265B-38
21	824	97.4	193	4	US-09-552-265B-38
22	824	97.4	193	4	US-09-552-265B-48
23	822	97.2	166	4	US-09-552-265B-20
24	822	97.2	166	4	US-09-552-265B-24
25	822	97.2	193	4	US-09-552-265B-36
26	822	97.2	193	4	US-09-552-265B-40
27	821	97.0	166	4	US-09-552-265B-26

Sequence 31, Appl
Sequence 42, Appl
Sequence 47, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 28, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 38, Appl
Sequence 49, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 37, Appl
Sequence 41, Appl
Sequence 27, Appl
Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-604-871-1

; Sequence 1, Application US/09604871
; Patent No. 6340742

; GENERAL INFORMATION:

; APPLICANT: Bug, Josef

; APPLICANT: Hilger, Bernd

; APPLICANT: Josel, Hans-Peter

; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

; FILE REFERENCE: 1098 nonprovisional

; CURRENT APPLICATION NUMBER: US/09/604,871

; CURRENT FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/151,454

; PRIOR FILING DATE: 1999-08-30

; PRIOR APPLICATION NUMBER: 60/147,452

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/142,243

; PRIOR FILING DATE: 1999-07-02

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 1

; LENGTH: 165

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-604-871-1

Query Match 100.0%; Score 846; DB 4; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.1e-99;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAENITTCABHCSLNENITVPDTKVNIFYAKRVEVGQQA 60

Db 1 APPRLICDSRVLYRLLEAKAENITTCABHCSLNENITVPDTKVNIFYAKRVEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPIQLHYDKAVSGIRSLTLLRALGAKQKAIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPIQLHYDKAVSGIRSLTLLRALGAKQKAIS 120

QY 121 PPDASAAPLRITATDTFRKLFVYSNFRGLKLYTGACRTGD 165

Db 121 PPDASAAPLRITATDTFRKLFVYSNFRGLKLYTGACRTGD 165

RESULT 2

US-09-604-938-1

; Sequence 1, Application US/09604938

; Patent No. 6583272

; GENERAL INFORMATION:

; APPLICANT: Bailon, Pascal

; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-938-1

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 3
US-08-318-193-70
Sequence 70, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-193-70

Query Match 100.0%; Score 846; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 4
US-09-604-871-2
Sequence 2, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/142,243
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 5
US-09-604-938-2

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: May 25, 2004, 11:15:13 ; Search time 58 Seconds
(without alignments)
803.799 Million cell updates/sec

title: US-09-830-964-1

effect score: 846

sequence: 1 APPRLCDSRVLELYLEAK.....SNFLRGLKLVGTGACRKTGD 165

scoring table: BLOSUM62

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otal number of hits satisfying chosen parameters: 1586107

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set-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

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1: Geneseqp19808.*

2: Geneseqp19908.*

3: Geneseqp20008.*

4: Geneseqp20018.*

5: Geneseqp20028.*

6: Geneseqp20038.*

7: Geneseqp20038s.*

8: Geneseqp20048.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	846	100.0	165	3	AAY93445 Amino aci
2	846	100.0	165	3	AAB03760 Human ery
3	846	100.0	165	3	AAY94605 Human ery
4	846	100.0	165	3	AAY99705 Non-glyco
5	846	100.0	165	4	AAB84525 Amino aci
6	846	100.0	165	4	ABB83621 Protein #
7	846	100.0	165	4	AAB66697 Human ery
8	846	100.0	165	5	AAM53061 Human ery
9	846	100.0	165	5	ABB77896 Amino aci
10	846	100.0	165	6	ABP98492 Amino aci
11	846	100.0	165	6	ABR39995 Human ery
12	846	100.0	166	1	AAP70398 Sequence
13	846	100.0	166	2	AAR23593 Recombina
14	846	100.0	166	2	AAM58404 Human ery
15	846	100.0	166	2	AAY77780 Human EPO
16	846	100.0	166	3	ABB07030 Modified
17	846	100.0	166	4	ABB83622 Protein #
18	846	100.0	166	4	AAE02641 Human ery
19	846	100.0	166	4	AAB66698 Human ery
20	846	100.0	166	5	ABG92101 Human ery
21	846	100.0	166	5	AAM53062 Human ery
22	846	100.0	166	5	ABB77897 Amino aci
23	846	100.0	166	6	ABR39996 Human ery
24	846	100.0	166	6	ABR57500 Human ery
25	846	100.0	167	1	AAP50299 Human rec

26	846	100.0	167	1	AAP50298
27	846	100.0	169	5	ABB77899 Amino aci
28	846	100.0	174	5	ABB77898 Amino aci
29	846	100.0	174	5	ABB77900 Amino aci
30	846	100.0	188	1	ABP60599 Clone lam
31	846	100.0	188	1	ABP81195 Erythrope
32	846	100.0	193	1	AAP50300 Human ery
33	846	100.0	193	1	AAP60597 Clone lam
34	846	100.0	193	1	AAP70256 Sequence
35	846	100.0	193	2	AAR65499 Human pre
36	846	100.0	193	2	AAR71137 Human ery
37	846	100.0	193	2	AAR74141 Human ery
38	846	100.0	193	2	AAR81982 Human ery
39	846	100.0	193	2	AAR98397 Human ery
40	846	100.0	193	3	AAY43398 Human ery
41	846	100.0	193	3	AAY94530 Human ery
42	846	100.0	193	3	AAY93638 Amino aci
43	846	100.0	193	3	AAY99704 Human non
44	846	100.0	193	4	AAB34978 Human ery
45	846	100.0	193	4	AAB85573 Human ery

ALIGNMENTS

RESULT 1
AAY93445
ID AAY93445 standard; protein; 165 AA.
XX
AC AAY93445;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of human erythropoietin.
XX
KW Human; erythropoietin; EPO; anaemia; renal failure.
XX
OS Homo sapiens.
XX
PN WO200028066-A1.
PD
PP 18-MAY-2000.
XX
PF 08-NOV-1999; 99WO-US026238.
XX
PR 06-NOV-1998; 98AR-00105609.
PR 23-FEB-1999; 99AR-00100679.
XX
(STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
PA Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376574/32.
XX
PT New host cell producing recombinant human erythropoietin (EPO) used for large scale production of EPO.
XX
PS Claim 1; Page 26-27; 51pp; English.
XX
CC The present sequence represents human erythropoietin protein. The specification describes a host cell line which is used to produce human erythropoietin (EPO). EPO is a glycoprotein. The cell line is used for the production of recombinant human erythropoietin. The protein is used for the treatment of anaemia, especially anaemia derived from renal failure
XX
SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPRLCDSRVLELYLEAKENITVPTKVNFWAKRMEVGGQA 60

Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120
121 PPDAASAAPLRTITADTFRKLFRVYSNLFGRGKLKLYTGACRTGD 165
121 PPDAASAAPLRTITADTFRKLFRVYSNLFGRGKLKLYTGACRTGD 165

RESULT 2
AA03760
ID AAB03760 standard; protein; 165 AA.
AC AAB03760;
XX 04-OCT-2000 (first entry)
XX Human erythropoietin (EPO) amino acid sequence.
XX Erythropoietin; EPO; human; erythroblast differentiation; anaemia;
XX large scale production; renal failure.
XX Homo sapiens.
XX WO200027997-A1.
XX 18-MAY-2000.
XX 08-NOV-1999; 95WO-US026240.
XX 06-NOV-1998; 98AR-00105611.
XX 23-FEB-1999; 99AR-00100681.
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376519/32.
XX A novel method for the massive culture of recombinant mammalian cells
XX producing recombinant human erythropoietin.
XX Example 8; Page 11-12; 23pp; English.
XX This sequence represents the human erythropoietin amino acid sequence.
XX Erythropoietin is a glycoprotein that stimulates erythroblast
XX differentiation in the bone marrow. The present invention relates to a
XX method for the large scale production of human EPO from recombinant
XX mammalian cells. The method comprises culturing mammalian cells which
XX express recombinant human EPO in culture medium comprising insulin.
XX Erythropoietin can be used to treat anaemia derived from renal failure.
XX The method allows for the industrial scale production of EPO, and
XX overcomes the problems of low reproducibility and output quality which
XX are encountered with previous production methods
XX Sequence 165 AA;
SQ Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNLFGRGKLKLYTGACRTGD 165

Db 121 PPDAASAAPLRTITADTFRKLFRVYSNLFGRGKLKLYTGACRTGD 165

RESULT 3
AA194605
ID AAY94605 standard; protein; 165 AA.
AC AAY94605;
XX 28-NOV-2000 (first entry)
XX Human erythropoietin.
XX Human; erythropoietin; EPO; purification; anaemia.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Modified-site 24 /note= "N-Glycosylation site"
XX Modified-site 38 /note= "N-Glycosylation site"
XX Modified-site 83 /note= "N-Glycosylation site"
XX Modified-site 126 /note= "N-Glycosylation site"
XX Modified-site /note= "O-Glycosylation site"
XX WO200027869-A1.
XX 18-MAY-2000.
XX 08-NOV-1999; 99WO-US026241.
XX 06-NOV-1998; 98AR-00105610.
XX 23-FEB-1999; 99AR-00100680.
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376485/32.
XX Novel methods for purifying recombinant human erythropoietin from
XX mammalian cell culture reagents.
XX Claim 16; Page 18; 30pp; English.
XX The present invention relates to a method for purifying erythropoietin
XX (EPO) for treatment of disease, especially anaemia. The method involves
XX treating cell culture supernatants with differential precipitation,
XX hydrophobic interaction chromatography, diafiltration, anionic and
XX cationic exchange chromatography and molecular exclusion chromatography.
XX The present sequence is the protein from the culture supernatant of
XX transfected cell lines after purification by the above process. The
XX sequence shows total homology with natural human EPO. The advantage of
XX this method is that high purity and quality EPO is produced. A further
XX advantage is that the process does not involve the use of organic
XX solvents that may harm the environment
XX Sequence 165 AA;
SQ Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRALGQAKAIS 120

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
QY 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165
Db 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 5

AAB84525
ID AAB84525 standard; protein; 165 AA.

XX AC AAB84525;
XX DT 05-SEP-2001 (first entry)

XX DE Amino acid sequence of human erythropoietin (EPO) protein.
XX KW Erythropoietin; EPO; erythropoietin stimulating protein; NESP;
XX OS Sustained release.

XX PN Homo sapiens.

XX PD WO200130320-A1.

XX PF 03-MAY-2001.

XX PR 23-OCT-2000; 2000WO-US029257.

XX PR 22-OCT-1999; 99US-00426566.

XX PR 13-OCT-2000; 2000US-00687981.

XX PA (AMGE-) AMGEN INC.

XX PI Burke P, Klumb L, Murphy K, Herberger J, French DL;

XX DR WPI; 2001-417552/44.

XX PT Sustained release composition comprises an active biological ingredient,
XX PT notably a protein or other biopolymer, particularly erythropoietin
XX PT stimulating protein, in biocompatible, biodegradable polymeric
XX PT microparticles.

XX PS Disclosure; Page 56; 61pp; English.

XX CC The present sequence encodes a human erythropoietin (EPO) protein. The
XX CC specification describes a composition for the sustained release of
XX CC biologically active EPO stimulating protein (NESP). The reduced frequency
XX CC of administration of NESP, which requires preferably injection by skilled
XX CC personnel, improves patient compliance. Also, sustained release reduces
XX CC the nature and severity of any side effects of the drug

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDVKVFNFKRMVEVGQQA 60
Db 1 APRRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDVKVFNFKRMVEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120

QY 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165

Db 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 6

Y 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165
b 121 PPDAASAAFLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 4

AA99705
D AA99705 standard; protein; 165 AA.

C C AAY99705;

T T 15-SEP-2000 (first entry)

E E Non-glycosylated erythropoietin analogue NGE-166delta.

X X Human; non-glycosylated erythropoietin analogue; NGEA; haematocrit;
X X antianaemic; anaemia; erythropoiesis promoter; mutant; mutin.

S S Homo sapiens.

S S Synthetic.

X X WO200032772-A2.

N N 08-JUN-2000.

D D 23-NOV-1999; 99WO-US027801.

F F 30-NOV-1998; 98US-0110289P.

X X (ELIL) LILLY & CO ELI.

I I Beals JM, Glaesner W, Micanovic R, Millican RL, Witcher DR;

X X WPI; 2000-412320/35.

R R N-PSDB; AAA48373.

X X Non-glycosylated erythropoietic compound useful for increasing hematocrit
X X level in mammal with insufficient hematocrit levels in conditions such as
X X anemia, comprises protein covalently bonded to polymer.

S S Claim 2; Page 93-94; 94pp; English.

X C The present sequence is a non-glycosylated erythropoietin analogue (NGEA)
X C designated NGE-166delta. The protein sequence is identical to the
X C sequence of wild-type human non-glycosylated erythropoietin NGE except
X C that Arg at position 166 is deleted. NGE promotes erythropoiesis and can
X C therefore be used to increase haematocrit levels in mammals with
X C conditions such as anaemia, in which levels of haematocrit are
X C insufficient. NGE analogues can also be used to treat such conditions.
X C NGEAs do not themselves cause a significant increase in haematocrit but
X C they acquire that property once they are derivatised with polyethylene
X C glycol polymers. The analogues can be produced using a linkerless
X C aldehyde modification process. They show stability and bioactivity in
X C vivo. The nucleotide sequence encoding this protein was constructed
X C synthetically by in vitro hybridisation using a set of six overlapping
X C oligonucleotides from the positive strand of human erythropoietin cDNA
X C with six complementary oligonucleotides (negative strand). The codon
X C usage was 100% optimised for E. coli codon usage. The hybridised
X C oligonucleotides were ligated with T4 DNA ligase and the ligation product
X C amplified by PCR. The nucleotide sequence was used to express the protein
X C in host cells

X Q Sequence 165 AA;

Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APRRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDVKVFNFKRMVEVGQQA 60

b 1 APRRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDVKVFNFKRMVEVGQQA 60

ABB83621
ID ABB83621 standard; protein; 165 AA.
XX
AC ABB83621;
XX
DT 10-OCT-2002 (first entry)
XX
DE Protein #1 relating to modified erythropoietin glycoprotein.
XX
KW Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
XX
DS Unidentified.
XX
PN NO200003372-A.
XX
PD 03-JAN-2001.
XX
PF 28-JUN-2000; 2000NO-00003372.
XX
PR 02-JUL-1999; 99US-0142254P.
XX
PR 23-AUG-1999; 99US-0150225P.
XX
PR 31-AUG-1999; 99US-0151548P.
XX
PR 17-NOV-1999; 99US-0166151P.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Bailon PS;
XX
DR WPI; 2001-135308/14.
XX
PT New conjugate having modified erythropoietin glycoprotein useful for
PT stimulating red blood cell production and for treating diseases
PT correlated with anemia in chronic renal failure, AIDS or cancer patients.
XX
PS Disclosure; Page 21-22; 30pp; Norwegian.
XX
CC This invention relates to new conjugate having a modified erythropoietin
CC glycoprotein, useful for stimulating red blood cell production, and for
CC treating or preventing diseases correlated with anaemia in chronic renal
CC failure, AIDS or cancer patients. The present sequence is a protein
CC related to the invention
XX
SQ Sequence 165 AA;
Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKMEVGGQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
RESULT 7
AAB66697
ID AAB66697 standard; protein; 165 AA.
XX
AC AAB66697;
XX
DT 06-APR-2001 (first entry)
XX
DE Human erythropoietin protein #1.
XX
KW Erythropoietin; EPO; reticulocytes; red blood cell; ethylene glycol;

KW chronic renal failure; AIDS; cancer.
XX
OS Homo sapiens.
XX
FN WO200102017-A2.
XX
PD 11-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-EP006009.
XX
PR 02-JUL-1999; 99US-0142243P.
XX
PR 05-AUG-1999; 99US-0147452P.
XX
PR 30-AUG-1999; 99US-0151454P.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Burg J, Hilger B, Josel H;
XX
DR WPI; 2001-147051/15.
XX
PT Novel erythropoietin-glycoprotein conjugate useful for treating diseases
PT correlated with anemia in chronic renal failure patients, AIDS and for
PT treating cancer, is linked to polyethylene glycol through linker.
XX
PS Claim 19; Fig 1; 40pp; English.
XX
CC The present invention relates to a conjugate comprising, human
CC erythropoietin glycoprotein (EPO) having at least one free amino group
CC and having in vivo biological activity of causing an increase the
CC production of reticulocytes and red blood cells, covalently linked to 1-3
CC lower-alkoxy poly(ethylene glycol) groups through a linker. The invention
CC is useful for preparation of medicaments for the treatment of prophylaxis
CC of disease correlated with anemia in chronic renal failure patients
CC (CRF), AIDS and for the treatment of cancer patients undergoing
CC chemotherapy
XX
SQ Sequence 165 AA;
Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKMEVGGQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
RESULT 8
AAM53061
ID AAM53061 standard; protein; 165 AA.
XX
AC AAM53061;
XX
DT 25-MAR-2002 (first entry)
XX
DE Human erythropoietin (hEPO), 165 residue form.
XX
KW Human; erythropoietin; EPO; hEPO; haemostatic; red blood cell;
KW blood disorder; anaemia; chronic renal failure; CRF; AIDS;
KW acquired immunodeficiency syndrome; cancer chemotherapy; haemostatic;
KW anti-HIV; antianaemic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

Disulfide-bond 7. 161
Modified-site 24 /note= "N-glycosylated"
Disulfide-bond 29. 33
Modified-site 38 /note= "N-glycosylated"
Modified-site 83 /note= "N-glycosylated"
Modified-site 126 /note= "N-glycosylated"
Modified-site 126 /note= "O-glycosylated"
WO200187329-A1.
22-NOV-2001.
08-MAY-2001; 2001WO-EP005187.
15-MAY-2000; 2000EP-00110355.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
Papadimitriou A;
WPI; 2002-082943/11.
Composition useful in the treatment of e.g. AIDS comprises an erythropoietin protein, and a multiple charged inorganic anion in a buffer.
Claim 28; Fig 1; 64pp; English.
The invention relates to liquid pharmaceutical compositions comprising an erythropoietin (EPO) protein, a multiple negatively charged inorganic anion in a buffer which maintains the pH of the solution from 5.5-7.0, and optionally at least one excipient. The erythropoietin used in the composition is preferably human (AAM53061 or AAM53062) a human erythropoietin variant containing additional glycosylation sites (AAM53064-AAM53107), or an erythropoietin with the C-terminal addition of a C-terminal fragment of human chorionic gonadotropin (AAM53063).
Erythropoietin is a glycoprotein essential for the formation of red blood cells and is therefore useful in the treatment of blood disorders characterised by low or defective red blood cell production. The compositions of the invention can be used in the treatment and prevention of anaemia in chronic renal failure patients (CRF), AIDS (acquired immunodeficiency syndrome), and/or for the treatment of cancer patients undergoing chemotherapy. Unlike prior art erythropoietin compositions, the compositions of the invention do not contain human serum albumin (thereby avoiding the possibility of viral infections and allergic reactions associated with this component), are liquid rather than lyophilisates (and therefore do not need to be reconstituted before administration), and are stable at elevated temperatures such as 25 degrees Celsius and even 40 degrees Celsius, and therefore can be stored without refrigeration for prolonged periods without degradation and loss of activity. The present sequence represents the 165 residue form of human erythropoietin which is specifically claimed for use in a composition of the invention
Sequence 165 AA;
Query Match 100.0%; Score 846; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86; Mismatches 0; Indels 0; Gaps 0;
Matches 165; Conservative 0;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNIFYAKRMEVQQA 60
Db 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTLLRALGQAEKIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTLLRALGQAEKIS 120
QY 121 PPDASAAPLRTITADTFKRLFRVYSNFRGLKLYTGCACTGD 165

RESULT 9

ABB77896
ID ABB77896 standard; protein; 165 AA.

XX ABB77896;

XX 07-OCT-2002 (first entry)

XX Amino acid sequence of a human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.

XX Homo sapiens.

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;

PI Wozny M;

XX WPI; 2002-566640/60.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
PT useful for treating diseases correlated with anaemia in chronic renal
PT failure patients and acquired immunodeficiency syndrome.

XX Claim 26; Fig 1; 40pp; English.

XX The present sequence represents a human erythropoietin (EPO) protein. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow

XX Sequence 165 AA;

Query Match 100.0%; Score 846; DB 5; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.3e-86;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNIFYAKRMEVQQA 60

Db 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNIFYAKRMEVQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTLLRALGQAEKIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTLLRALGQAEKIS 120

Db 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGD 165

QY 61 VEVNQG LALISEAVLRQGLLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

b 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSLTLLRALGAKQKEAIS 120
 y 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165
 b 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165

RESULT 12
 AP70398
 D AAP70398 standard; protein; 166 AA.
 C AAP70398;
 K
 X I 19-FEB-1991 (first entry)
 X Sequence of human erythropoietin (EPO).
 E Mega-karyocyte-platelet growth factor; hormone;
 M mega-karyocyte colony stimulating factor; therapy;
 M small acetyl cholinesterase positive cell; erythrocyte growth effect.
 K Homo sapiens.
 S
 X JP62149624-A.
 N 03-JUL-1987.
 D
 X 15-AUG-1986; 86JP-00191542.
 F
 X 13-SEP-1985; 85JP-00203049.
 R (KAWA/) KAWAKITA M.
 X WPI; 1987-224837/32.
 X Megakaryocyte-platelet growth factor - contains as active component human erythropoietin and is used to treat diseases caused by decrease in platelets.
 T Disclosure; Page 181; 8pp; Japanese.
 S
 X All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-platelet growth factor contains human EPO as an active principle. Human EPO has a megakaryocyte colony-stimulating activity and increases the ratio of small acetyl cholinesterase positive cell (SACH+), which is immature megakaryocyte. Human EPO effects megakaryocyte-platelet system other than an erythrocyte growth effect. Megakaryocyte-platelet growth is usable as a remedy for diseases caused by a platelet decrease

Query Match 100.0%; Score 846; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 APRLICDSRVLYLLEAKEAENITTCGAECSLNENITVPDTKVNFYAWKRMVEVGQQA 60
 b 1 APRLICDSRVLYLLEAKEAENITTCGAECSLNENITVPDTKVNFYAWKRMVEVGQQA 60
 y 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSLTLLRALGAKQKEAIS 120
 b 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSLTLLRALGAKQKEAIS 120
 y 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165
 b 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165

RESULT 13
 AAP70398
 D AAP70398 standard; protein; 166 AA.
 X

AC AAR23593;
 XX 20-OCT-1992 (first entry)
 DT Recombinant hematopoietic molecule portion 2.
 XX Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis.
 KW Homo sapiens.
 XX OS
 XX PN W09206116-A.
 XX PD 16-APR-1992.
 XX PF 26-SEP-1991; 91WO-US007053.
 XX PR 28-SEP-1990; 90US-00589958.
 XX PA (ORTH) ORTHO PHARM CORP.
 XX PI Rosen JJ;
 XX WPI; 1992-150819/18.
 DR Recombinant hematopoietic molecules useful in treating anaemia(s) - comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity.
 XX Disclosure; Page 32; 82pp; English.
 CC This protein sequence given comprises the entire amino acid sequence of human erythropoietin (EPO). EPO leads to the maturation of erythrocytes and is therefore designated as a late myeloid differentiation factor (MDF). Within the scope of the invention hybrid molecules were produced which contain at least a portion of an early MDF and at least a portion of a late MDF covalently linked. The EPO sequence given is effective within the scope of the invention in full or in a truncated version.
 CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg. IL-3. These compounds can be used to promote hematopoiesis in a patient. The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDA to act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins eg. renal failure and AIDS. It is easier to produce and administer one recombinant molecule rather than two separate molecules

Sequence 166 AA;
 Query Match 100.0%; Score 846; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRLICDSRVLYLLEAKEAENITTCGAECSLNENITVPDTKVNFYAWKRMVEVGQQA 60
 Db 1 APRLICDSRVLYLLEAKEAENITTCGAECSLNENITVPDTKVNFYAWKRMVEVGQQA 60
 Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSLTLLRALGAKQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSLTLLRALGAKQKEAIS 120
 Qy 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165
 Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKILKLYTGEACRTGD 165

RESULT 14
 AAW58404
 ID AAW58404 standard; protein; 166 AA.
 XX AAW58404;
 AC AAW58404;
 XX 12-OCT-1998 (first entry)
 DT

CC DE Human erythropoietin.
CC DE Erythropoietin receptor agonist; EPO; human; anaemia;
CC GW haematopoietic deficiency; red blood cell; erythroid progenitor;
CC GW bone marrow suppression.
CC XS Homo sapiens.
CC NN WO9818926-A1.
CC ND 07-MAY-1998.
CC FE 23-OCT-1997; 97WO-US018703.
CC PR 25-OCT-1996; 96US-0034044P.
CC PA (SEAR) SEARLE & CO G D.
CC PI McWherter CA, Feng Y, Summers N;
CC PR WPI; 1998-272221/24.
CC PR N-PSDB; AAV31031.
CC PT Human erythropoietin receptor agonist polypeptide - used to stimulate the
CC PT production of red blood cells in a patient.
CC XS Claim 1; Page 93; 112pp; English.
CC CC A claimed human erythropoietin (EPO) receptor agonist polypeptide
CC CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
CC CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
CC CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
CC CC directly or through a linker (see AAW58405-12) capable of joining the N-
CC CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
CC CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
CC CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
CC CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
CC CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
CC CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
CC CC molecules (see AAV30971-V11030) encoding novel EPO receptor agonists; a
CC CC method of producing an EPO receptor agonist using transformed or
CC CC transfected host cells; and methods for stimulating the production of
CC CC haematopoietic cells, for selective ex vivo expansion of erythroid
CC CC progenitors, and treating patients having a haematopoietic disorder using
CC CC the EPO receptor agonists. The EPO receptor agonists retain one or more
CC CC activities of native EPO and may also show improved haematopoietic cell-
CC CC stimulating activity and/or an improved activity profile which may
CC CC include reduction of undesirable biological activities associated with
CC CC native EPO and/or have improved physical properties such as increased
CC CC solubility, stability and refold efficiency
CC XX Sequence 166 AA;
SQ Query Match 100.0%; Score 846; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLYLLAKEAENITTCGAEHCSLNENITVPDTKVFYAWKMEVQQA 60
DB 1 APPRLICDSRVLYRLLYLLAKEAENITTCGAEHCSLNENITVPDTKVFYAWKMEVQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDAKAVSLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDAKAVSLRSLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRITTTADTRKLFVRYVSNFLRGLKLYTGEACRTGD 165
DB 121 PPDAASAPLRITTTADTRKLFVRYVSNFLRGLKLYTGEACRTGD 165
RESULT 15
AAW77780

ID XX AAW77780 standard; protein; 166 AA.
AC AAW77780;
XX 24-NOV-1998 (first entry)
DT Human EPO receptor agonist polypeptide.
DE Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
XX human; chimeric protein; stem cell expansion; tumour; infection;
KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
XX Homo sapiens.
OS Key Location/Qualifiers
XX Misc-difference 1..6 /note= "1-6 amino acids of the N-terminus are optionally
FT deleted"
FT Misc-difference 23..24 /note= "possible positions of new C- and N-termini"
FT Misc-difference 24..25 /note= "possible positions of new C- and N-termini"
FT Misc-difference 25..26 /note= "possible positions of new C- and N-termini"
FT Misc-difference 26..27 /note= "possible positions of new C- and N-termini"
FT Misc-difference 27..28 /note= "possible positions of new C- and N-termini"
FT Misc-difference 28..29 /note= "possible positions of new C- and N-termini"
FT Misc-difference 29..30 /note= "possible positions of new C- and N-termini"
FT Misc-difference 30..31 /note= "possible positions of new C- and N-termini"
FT Misc-difference 31..32 /note= "possible positions of new C- and N-termini"
FT Misc-difference 32..33 /note= "possible positions of new C- and N-termini"
FT Misc-difference 33..34 /note= "possible positions of new C- and N-termini"
FT Misc-difference 34..35 /note= "possible positions of new C- and N-termini"
FT Misc-difference 35..36 /note= "possible positions of new C- and N-termini"
FT Misc-difference 36..37 /note= "possible positions of new C- and N-termini"
FT Misc-difference 37..38 /note= "possible positions of new C- and N-termini"
FT Misc-difference 38..39 /note= "possible positions of new C- and N-termini"
FT Misc-difference 39..40 /note= "possible positions of new C- and N-termini"
FT Misc-difference 40..41 /note= "possible positions of new C- and N-termini"
FT Misc-difference 41..42 /note= "possible positions of new C- and N-termini"
FT Misc-difference 42..43 /note= "possible positions of new C- and N-termini"
FT Misc-difference 43..44 /note= "possible positions of new C- and N-termini"
FT Misc-difference 44..45 /note= "possible positions of new C- and N-termini"
FT Misc-difference 45..46 /note= "possible positions of new C- and N-termini"
FT Misc-difference 46..47 /note= "possible positions of new C- and N-termini"
FT Misc-difference 47..48 /note= "possible positions of new C- and N-termini"
FT Misc-difference 48..49 /note= "possible positions of new C- and N-termini"
FT Misc-difference 49..50 /note= "possible positions of new C- and N-termini"
FT Misc-difference 50..51 /note= "possible positions of new C- and N-termini"

Misc-difference 127. .128
FT /note= "possible positions of new C- and N-termini"
FT 128. .129
Misc-difference 128. .129
FT /note= "possible positions of new C- and N-termini"
FT 129. .130
Misc-difference 129. .130
FT /note= "possible positions of new C- and N-termini"
FT 130. .131
Misc-difference 130. .131
FT /note= "possible positions of new C- and N-termini"
FT 131. .132
Misc-difference 131. .132
FT /note= "possible positions of new C- and N-termini"
FT 162. .166
Misc-difference 162. .166
FT /note= "1-5 amino acids of the C-terminus are optionally
FT deleted".
FT
WO9817810-A2.
DN
XX
XX
30-APR-1998.
ED XX
PF XX
23-OCT-1997; 97WO-USO20037.
PP XX
XX
25-OCT-1996; 96US-0029629P.
PR XX
XX
(SEAR) SEARLE & CO G D.
PA
XX
McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
PI
WPI; 1998-261504/23.
DR
XX
Multi-functional chimeric haematopoietic receptor agonist - useful to
PT treat haematopoietic disorders, tumours, infections or autoimmune
FT diseases.
XX
Claim 1; Page 762; 84lpp; English.

A human erythropoietin (EPO) receptor agonist polypeptide comprises a modified EPO amino acid sequence of the formula provided in AAW7780, in which the N-terminus is joined to the C-terminus directly or via a linker, the polypeptide having new C- and N-termini at one of the positions indicated. Novel claimed multi-functional chimeric haematopoietic receptor agonists (see AAW77812-22) have the formula R1-L1-R2, R2-L1-R1, R1-R2 or R2-R1, where L is a linker and R1 and R2 are independently selected from: (a) the human EPO receptor agonist; (b) a human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a human fit-3 receptor agonist polypeptide (see AAW77782); (d) a modified human granulocyte colony stimulating factor (G-CSF) polypeptide (see AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784); (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a factor selected from the group consisting of a CSF, a cytokine, a lymphokine, an interleukin and a haematopoietic growth factor, provided that at least R1 or R2 is selected from (a), (b) or (c) as above. The multi-functional chimeric haematopoietic receptor agonist can be used to stimulate the production of haematopoietic cells in a patient, for the ex vivo expansion of haematopoietic cells, for the production of dendritic

Search completed: May 25, 2004, 11:21:35

Job time : 59 secs



Sequence 2, Application US/09604938
Patent No. 6583272
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-604-938-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 6
IS-09-462-941-2
Sequence 2, Application US/09462941
Patent No. 6608183
GENERAL INFORMATION:
APPLICANT: Cox III, George N
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-462-941-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 7
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; PCT-US94-04361-37

Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNLENITVPDTKVNFYAWKMEVGQQA 60
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
121 PPDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 8
US-07-903-220-1
; Sequence 1, Application US/07903220
; Patent No. 5322837

ue May 23 12.51.31 2004

ue 03 030 301

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; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
; TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul H. Heller
; STREET: Kenyon & Kenyon, One Broadway
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-07-903-220-1

; Query Match 100.0%; Score 846; DB 1; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLRGLKLYTGEACRTGD 192

; RESULT 9
; US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2

; Query Match 100.0%; Score 846; DB 4; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 120

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34

; Query Match 100.0%; Score 846; DB 2; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLRGLKLYTGEACRTGD 192

; RESULT 10
; US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 655343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Hennen, Dennis, J.
; TITLE OF INVENTION: No. 655343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057CPL
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307 ←
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4

; Query Match 100.0%; Score 846; DB 4; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDKAVSGLRSLTLLRALGAKQEAIS 120
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Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147
QY 121 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 165
Db 148 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 192

RESULT 11

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: No. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8

Query Match 99.6%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 2.6e-99;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGGQA 60
Db 1 APRLLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 165
Db 121 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 165

RESULT 12

US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu

; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34

Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 1.1e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGGQA 60
Db 233 APRLLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGGQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 352
QY 121 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 165
Db 353 PPDAAASAPLRTITADTPRKLFRVYSNFRGLRGLKLYTGEACRTGD 397

RESULT 13

US-08-809-156B-34
; Sequence 34, Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6472204uto
; Hashino, Kimikazu
; Koyama, No. 6472204uto
; Hashino, Kimikazu
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET

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QY      121 PPDAASAPLRIITTAOTFRKLFVYS  
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        |  
Db      148 PPDAASAPLRIITTAOTFRKLFVYS
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Search completed: May 25, 2004, 11:24:06
Job time : 24 secs